



```

1 CCATTCCAAA CAAGTCAGGA AAGCCTGCAC AGGACTGGAT AAATAATTAA
51 GAACAGAGTG TTCTGAACAT CAACACAAAG TGGAAGAACC TTAAGCTGAA
101 GGTACAGTAT ATTATTACA CTGAAGGGGC TTGTGTGTGG ACAAGAAAGC
151 GCTGACAGCT CAAATGGATC CCATGGAAC TGAAGAAATGTC AACATCGAAC
201 CAGATGATGA GAGCAGCAGT GGAGAAAGTG CTCCAGATAG CTACATCAGG
251 ATAGGAAATT CAGAAAAGGC AGCAATGAGC AGTCAATTTG CTAATGAAGA
301 CACTGAAAGT CAGAAATTCC TGACAAATGG ATTTTGGGG AAAAAGAAGC
351 TGGCAGATTA TGCTGATGAA CACCATCCCG GAACCACTTC CTTTGAATG
401 TCTTCATTTA ACCTGAGTAA TGCCATCATG GGCAGTGGGA TCCTGGGCTT
451 GTCCTATGCC ATGGCCTACA CAGGGGTCAT ACTTTTATA ATCATGCTGC
501 TTGCTGTGGC AATATTATCA CTGTATTGAG TTCACCTTTT ATTAATAACA
551 GCCAAGGAAG GAGGGTCTTT GATTTATGAA AAATTAGGAG AAAAGGCATT
601 TGGATGGCCG GGAAAAATTG GAGCTTTTGT TTCCATTACA ATGCAGAACA
651 TTGGAGCAAT GTCAAGCTAC CTCTTTATCA TTAAATATGA ACTACCTGAA
701 GTAATCAGAG CATTGATGGG ACTTGAAGAA AATACTGGAG AATGGTACCT
751 CAATGGCAAC TACCTCATCA TATTTGTGTC TGTGGAATT ATTCTTCCAC
801 TTTGCTCCT TAAAAATTTA GGTATCTTG GCTATACCAG TGGATTTTCT
851 CTTACCTGCA TGGTGTTTT TGTTAGTGTG GTGATTTACA AGAAATTCCA
901 AATACCCTGC CCTCTACCTG TTTTGGATCA CAGTGTGGA AATCTGTCAT
951 TCAACAACAC GCTTCCAATG CATGTGGTAA TGTTACCCAA CAACTCTGAG
1001 AGTTCTGATG TGAACCTCAT GATGGATTAC ACCCACCACA ATCCTGCAGG
1051 GCTGGATGAG AACCAGGCCA AGGGCTCTCT TCATGACAGT GGAGTAGAAT
1101 ATGAAGCTCA TAGTGATGAC AAGTGTGAAC CCAAATACTT TGTATTCAAC
1151 TCCCGGACGG CCTATGCAAT TCCTATCCTA GTATTTGCTT TTGTATGCCA
1201 CCCTGAGGTC CTTCCCATCT ACAGTGAAC TAAAGATCGG TCCCGGAGAA
1251 AAATGCAAAC GGTGTCAAAT ATTTCCATCA CGGGGATGCT TGTGATGTAC
1301 CTGCTTGCCG CCCTCTTTGG TTACCTAACC TTCTATGGAG AAGTTGAAGA
1351 TGAATTACTT CATGCCTACA GCAAAGTGTA TACATTAGAC ATCCCTCTTC
1401 TCATGGTTG CCTGGCAGTC CTTGTGGCAG TAACACAAAC TGTGCCATT
1451 GTCCTCTTCC CAATTCGTAC ATCAGTGATC AACTGTTAT TTCCCAAACG
1501 ACCCTTCAGC TGGATACGAC ATTTCTCTGAT TGCAGCTGTG CTTATTGCAC
1551 TTAATAATGT TCTGGTCATC CTTGTGCCAA CTATAAAATA CATCTTCGGA
1601 TTCATAGGGG CTTCTTCTGC CACTATGCTG ATTTTATTC TTCCAGCAGT
1651 TTTTATCTT AAACCTGTCA AGAAAGAAAC TTTTAGGTCA CCCCCAAAGG
1701 TCGGGGCTTT AATTTTCTT GTGGTTGGAA TATCTTCAT GATTGGAAGC
1751 ATGGCACTCA TTATAATTGA CTGGATTTAT GATCCTCCAA ATTCCAAGCA
1801 TCACTAACAC AAGGAAAAAT AC (SEQ ID NO:1)

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FEATURES:

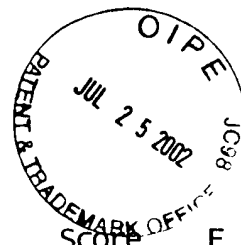
5'UTR: 1-163
 Start Codon: 164
 Stop Codon: 1805
 3'UTR: 1808

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FIGURE 1A



HOMOLOGOUS PROTEINS:

Top BLAST Hits:

			Score	E
CRA 145000039337444	/altid=gi 12017941	/def=gb AAG45335.1 AF295...	975	0.0
CRA 114000033649823	/altid=gi 10945621	/def=gb AAG24618.1 AF298...	597	e-169
CRA 160000003782430	/altid=gi 8677401	/def=gb AAF75589.2 AF1736...	591	e-168
CRA 148000002720069	/altid=gi 8248427	/def=gb AAF74195.1 AF2496...	587	e-166
CRA 87000000006802	/altid=gi 7243145	/def=dbj BAA92620.1 (AB03...	578	e-164
CRA 18000005069115	/altid=gi 5870893	/def=ref NP_006832.1 tran...	500	e-140
CRA 88000001154721	/altid=gi 7406950	/def=gb AAF61849.1 AF15985...	496	e-139
CRA 66000019404613	/altid=gi 9506837	/def=ref NP_061849.1 amin...	495	e-139
CRA 100000004435450	/altid=gi 8926332	/def=gb AAF81797.1 AF2730...	492	e-138
CRA 335001098689635	/altid=gi 11434147	/def=ref XP_006635.1 hy...	480	e-134

EST:

gi 10934204	/dataset=dbest /taxon=96...	1072	0.0
gi 10286121	/dataset=dbest /taxon=96...	718	0.0
gi 9872634	/dataset=dbest /taxon=960...	680	0.0
gi 2656674	/dataset=dbest /taxon=9606 ...	549	e-154
gi 9882497	/dataset=dbest /taxon=960...	541	e-151
gi 689641	/dataset=dbest /taxon=9606 /...	525	e-147

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

Expression information from BLAST dbEST hits:

gi|10934204 whole embryo (mainly head)
 gi|10286121 Hepatocellular carcinoma
 gi|9872634 Non-cancerous liver
 gi|2656674 Fetal liver spleen
 gi|9882497 Non cancerous liver
 gi|689641 Liver

Expression information from PCR-based tissue screening panels:

Mixed tissue (Brain, Heart, Kidney, Lung, Spleen, Testis, Leukocyte)

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FIGURE 1B



1 MDPMELRNVN IEPDDESSG ESAPDSYIRI GNSEKAAMSS QFANEDTESQ
 51 KFLTNGFLGK KKLADYADEH HPGTTSFGMS SFNLSNAIMG SGILGLSYAM
 101 AYTGVILFII MLLAVAILSL YSVHLLKTA KEGGSLIYEK LGEKAFGWPG
 151 KIGAFVSITM QNIGAMSSYL FIIKYELPEV IRAFMGLEEN TGEWYLNNGY
 201 LIIFVSVGII LPLSLLKNLG YLGYSFGFSL TCMVFFVSVV IYKKFQIPCP
 251 LPVLDHSVGN LSFNNTLPMH VMPLPNNSSE SDVNFMDYT HRNPAGLDEN
 301 QAKGSLHDSG VEYEAHSDDK CEPKYFVFNS RTAYAIPILV FAFVCHPEVL
 351 PIYSELKDRS RRRKMQTVSNI SITGMLVMYL LAALFGYLTG YGEVEDELLH
 401 AYSKVYTLDI PLLMVRLAVL VAVTQTVPIV LFPRTSVIT LLFPRKPFWS
 451 IRHFLIAAVL IALNNVLVIL VPTIKYIFGF IGASSATMLI FILPAVFYLK
 501 LVKKETFRSP QKVGALIFLV VGIFFMIGSM ALIIDIWIYD PPNSKHH (SEQ ID NO:2)

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION

N-glycosylation site

Number of matches: 5

- 1 83-86 NLSN
- 2 260-263 NLSF
- 3 264-267 NNTL
- 4 276-279 NNSE
- 5 369-372 NISI

[2] PDOC00004 PS00004 CAMP_PHOSPHO_SITE

CAMP- and cGMP-dependent protein kinase phosphorylation site

503-506 KKET

[3] PDOC00005 PS00005 PKC_PHOSPHO_SITE

Protein kinase C phosphorylation site

Number of matches: 7

- 1 33-35 SEK
- 2 49-51 SQK
- 3 129-131 TAK
- 4 290-292 THR
- 5 360-362 SRR
- 6 473-475 TIK
- 7 506-508 TFR

[4] PDOC00006 PS00006 CK2_PHOSPHO_SITE

Casein kinase II phosphorylation site

Number of matches: 5

- 1 18-21 SSGE
- 2 22-25 SAPD
- 3 129-132 TAKE
- 4 305-308 SLHD
- 5 309-312 SGVE

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FIGURE 2A

Docket No.: CL001010

Serial No.: 09/776,705

Inventor: Karl GUEGLER et al.

Title: ISOLATED HUMAN TRANSPORTER PROTEINS...



[5] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 6

1	95-100	GLSYAM
2	153-158	GAFVSI
3	164-169	GAMSSY
4	186-191	GLEENT
5	296-301	GLDENQ
6	482-487	GASSAT

[6] PDOC00009 PS00009 AMIDATION
Amidation site

58-61 LGKK

Membrane spanning structure and domains:

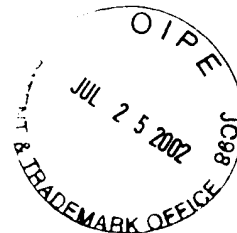
Helix	Begin	End	Score	Certainty
1	79	99	1.125	Certain
2	102	122	2.503	Certain
3	153	173	1.197	Certain
4	197	217	1.785	Certain
5	222	242	2.123	Certain
6	332	352	1.240	Certain
7	370	390	2.166	Certain
8	414	434	1.301	Certain
9	453	473	1.520	Certain
10	476	496	2.166	Certain
11	515	535	2.628	Certain

FIGURE 2B

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BLAST Alignment to Top Hit:

>CRA|145000039337444 /altid=gi|12017941
/def=gb|AAG45335.1|AF295535_1 (AF295535) amino acid
transporter system A3 [Rattus norvegicus] /org=Rattus
norvegicus /taxon=10116 /dataset=nraa /length=547
Length = 547

Score = 975 bits (2492), Expect = 0.0
Identities = 478/547 (87%), Positives = 508/547 (92%)

Query: 1 MDPMELRNVNIEPDDSSSGESAPDSYIRIGNSEKAAMSSQFANEDTESQKFLTNGFLGK 60
MDP+ELR+VNIEP ++S S +S Y +GNSEK AM SQFANED ESQKFLTNGFLGK
Sbjct: 1 MDPIELRSVNIEPYEDSCSVDSIQSCYTGMGNSEKGMDSQFANEDAESQKFLTNGFLGK 60

Query: 61 KKLADYADEHHPGTTSFGMSSFNLNSNAIMGSGILGLSYAMAYTGVLFIIMLLAVAILSL 120
K L DYADEHHPGTTSFGMSSFNLNSNAIMGSGILGLSYAMA TG++LF+IMLL VAILSL
Sbjct: 61 KTLTDYADEHHPGTTSFGMSSFNLNSNAIMGSGILGLSYAMANTGIVLFVIMLLTVAILSL 120

Query: 121 YSVHLLLKTAKEGGS LIYEKLGEKAFGWPGKIGAFVSITM QNIGAMSSYLFIKYELPEV 180
YSVHLLLKTAKEGGS LIYEKLGEKAFGWPGKIGAF+SITM QNIGAMSSYLFIKYELPEV
Sbjct: 121 YSVHLLLKTAKEGGS LIYEKLGEKAFGWPGKIGAFISITM QNIGAMSSYLFIKYELPEV 180

Query: 181 IRAFMGLEENTGEWYLN GNLYIIFVSVGIILPLSLLKNLGYLGYTSGFSLTQWFFVSW 240
IR FMGLEENTGEWYLN GNLY++FVSVGIILPLSLLKNLGYLGYTSGFSLTQWFFVSW
Sbjct: 181 IRVFMGLEENTGEWYLN GNLYLVFVSVGIILPLSLLKNLGYLGYTSGFSLTQWFFVSW 240

Query: 241 IYKKFQIPCLPLVLDHSGVGNLSFNNTLPMHVMLPNNSESSDVNFMDYTHRNPAGLDEN 300
IYKKFQIPCLPLVLDH+ GNL+FNNTLPMHV+MLPNNSES+ +NFM+DYTHR+P GLDE
Sbjct: 241 IYKKFQIPCLPLVLDHNNGNLTFNNTLPMHVIMLPNNSESTGMNFMVDYTHRDPEGLDEK 300

Query: 301 QAKGSLHDSGVEYEAHSDDKCEPKYFVFNSTAYAIPIILVFAFVCHPEVLPIYSELKDORS 360
A G LH SGVEYEAHS DKC+PKYFVFNSTAYAIPIIL FAFVCHPEVLPIYSELKDORS
Sbjct: 301 PAAGPLHGSGVEYEAHSGDKCQPKYFVFNSTAYAIPIILAFVCHPEVLPIYSELKDORS 360

Query: 361 RRKMQTVSNISITGMLV MYLLAALFGYLTFYGEVEDELLHAYSKVYTLDIPLLMVRLAVL 420
RRKMQTVSNISITGMLV MYLLAALFGYL+FYGEVEDELLHAYSKVYT D LLMVRLAVL
Sbjct: 361 RRKMQTVSNISITGMLV MYLLAALFGYLSFYGEVEDELLHAYSKVYTFDTALLMVRLAVL 420

Query: 421 VAVTQTVPIVLFP IRTSVITLLFPKRPFWSIRHFLIAAVLIALNNVLVILVPTIKYIFGF 480
VAVT TVPIVLFP IRTSVITLLFP+RPFSW++HF IAA++IALNNVLVILVPTIKYIFGF
Sbjct: 421 VAVTLTVPIVLFP IRTSVITLLFPRRPFWSWKHFGIAAIIIALNNVLVILVPTIKYIFGF 480

Query: 481 IGASSATMLIFILPAV FYLKL VKKETFRSPQKVGALIFLVGIFFMIGSMALIIIDWIYD 540
IGASSATMLIFILPA FYLKL VKKE RSPQK+GAL+FLV GI FM+GSMALIIIDWIY+
Sbjct: 481 IGASSATMLIFILPAAFY LKL VKKEPLRSPQKIGALVFLVTGIIFMIGSMALIIIDWIYN 540

Query: 541 PPN SKHH 547
PPN HH
Sbjct: 541 PPNPDHH 547 (SEQ ID NO :4)

>CRA|114000033649823 /altid=gi|10945621
/def=gb|AAG24618.1|AF298897_1 (AF298897) amino acid
transporter system A [Homo sapiens] /org=Homo sapiens

FIGURE 2C

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/taxon=9606 /dataset=nraa /length=506
Length = 506



Score = 597 bits (1522), Expect = e-169
Identities = 315/549 (57%), Positives = 383/549 (69%), Gaps = 46/549 (8%)

Query: 1 MDPMELRNVNIEPDDESSSGESAPD---SYIRIGNSEKAAMSSQFANEDTESQKFLTNGF 57
M E+ +I PD++SSS S D SY +++AA+ S +A+ D E+Q FL
Sbjct: 1 MKKAEMGRFSISPDEDSSSYSSNSDFNYSY-----PTKQAALKSHYADVDPENQNFLLSN 56

Query: 58 LGKKKLADYADEHHPGTTSTFGMSSFNLNAIMGSGILGLSYAMAYTGVLFIIMLLAVAI 117
LGKKK Y E HPGTTSTFGMS FNLSNAI+GSGILGLSYAMA TG+ LFII+L V+I
Sbjct: 57 LGKKK---YETEFHPGTTSTFGMSVFNLSNAIVGSGILGLSYAMANTGIALFIILLTFVSI 113

Query: 118 LSLYSVHLLLKTAKEGGSLIYEKLGEKAFGWPGKIGAFVSITMQNIGAMSSYLFIIKYEL 177
SLYSVHLLLKTA EGGSL+YE+LG KAFG GK+ A SITMQNIGAMSSYLF+KYEL
Sbjct: 114 FSLYSVHLLLKTANEGGSLLYEQLGYKAFGLVGKLAASGSITMQNIGAMSSYLFIVKYEL 173

Query: 178 PEVIRAFMGLEENTGEWYLNNGNYLIIFVSVGIILPLSLLKNLGYLGYTSGFSLTOMVFFV 237
P VI+A +E+ TG WYLNNGNYL++ VS+ +ILPLSL +NLGYLGYTSG SL OMVFF+
Sbjct: 174 PLVIQALTNIEDKTGLWYLNNGNYLVLLVSLVILPLSLFRNLGYLGYTSGLSLLOMVFFL 233

Query: 238 SVWIYKKFQIPCPPLVLDHSVGNLSFNNTLPMHVMPLPNSESSDVNFMDYTHRNPAGL 297
VVI KKFQ+PCP+ + N + N TL ++P
Sbjct: 234 IIVICKKFQVPCPVEAA--LIINETINTLTQTALVP----- 269

Query: 298 DENQAKGSLHDSGVEYEAHSDDKCEPKYFVFNSTAYAIPILVFAFVCHPEVLPIYSELK 357
+ + +D C P YF+FNS+T YA+PIL+F+VCHP VLPIY ELK
Sbjct: 270 -----ALSHNVTENDSCRPHYFIFNSQTVYAVPILIFSVCHPAVLPIYEELK 317

Query: 358 DRSRRKMQTVSNISITGMLVMYLLAALFGYLTFYGEVEDELLHAYSKVYTLDIPLLMVRL 417
DRSRR+M VS IS M +MYLLAALFGYLTFY VE ELLH YS + DI LL+VRL
Sbjct: 318 DRSRRRMNVSKISFFAMFLMYLLAALFGYLTFYEHVESELLHTYSSILGTDILLIVRL 377

Query: 418 AVLVAVTQTVPIVLFPRTSVITLLFPKRPFSWIRHFLIAAVLIALNNVLVILVPTIKYI 477
AVL+AVT TVP+V+FPIR+SV LL + FSW RH LI ++A N+LVI VPTI+ I
Sbjct: 378 AVLMAVTLTVPWIFPIRSSVTHLLCASKDFSWRHSILITVSILAFTNLLVIFVPTIRDI 437

Query: 478 FGFIGASSATMLIFILPAVFYKLKVKKETFRSPQKVGALIFLVGIFFMIGSMALIIDW 537
FGFIGAS+A+MLIFILP+ FY+KLVKKE +S QK+GAL FL+ G+ M GSMALI++DW
Sbjct: 438 FGFIGASAASMLIFILPSAFYIKLVKKEPKSVQKIGALFFLLSGVLVMTGSMALIVLDW 497

Query: 538 IYDPPNSKH 546
+++ P H
Sbjct: 498 VHNAPGGGH 506 (SEQ ID NO :5)

Hmmer search results (Pfam):

Model	Description	Score	E-value	N
PF01490	Transmembrane amino acid transporter protein	187.0	2.9e-52	2
CE00398	E00398 CD53	4.0	4.8	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
CE00398	1/1	90	110 ..	1	23 [.	4.0	4.8

FIGURE 2D

Docket No.: CL001010
Serial No.: 09/776,705
Inventor: Karl GUEGLER et al.

Title: ISOLATED HUMAN TRANSPORTER PROTEINS...

PF01490	1/2	99	236 ..	1	179 [.	58.9	2.5e-14
PF01490	2/2	305	529 ..	200	467 .]	133.9	3e-36



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FIGURE 2E



1 AGCTTAGCAA TATGGATCAA GAGGTCCAAT ACCTGATTAA TAAAAGTTTC
 51 AGGAGTAAAC AAAGGGGAAG AAATAGTTTT TTAAATAGT AGAACTTTTT
 101 TTATTTTGTAG AAAATGTGTC TTCTATAGAA GAAAGACAAG CCTTTTGATT
 151 GGGCCGCTCTG CATGCTGAGT ATGATGAATT TAAAAGCGA CTCACATCTA
 201 GTCACGTCGT GATGAAAGGA TAAGGATAAA AATTCTGAAA TCCTCAGAAA
 251 ACCATCGATA AATTATCTAT AAAGAAATAA GAGCCAGACT CATCAATAGA
 301 AGCTAGAAGA GAGAAGTTTC TTCAATATTC TGAAGGAAAA TGCTTCTGAA
 351 TCTAGAATTC AAACAATTAA CAAAGTTTGA AGGCAAAATA AAGAATTTTC
 401 CAACATGAAG CAACTCAGAA ATTCTATTTA CAGACATAGG CTCATTGTGT
 451 GAAAAAGTT ATTCAAGGCA TTATTTTAGC ATAATGCAAA ATAAACTGAA
 501 GAAAGAAGAT AGAATGCCGT TCAAGAACT AGCAGCTGAG CAAGACTCAG
 551 AGGTTGGAGG AGGAAGCCAT TCAGAATGAG AAAGAGCATA GAAAATTTGC
 601 TTTCAAAGTT TTGGTAATAT AGAATTATAT TTCACTTATT ATGTAGTCAA
 651 ATACACCACT TTGTCTTTAG GGCATACTAT TTATACAGTG ATAATACTGT
 701 AATTGCTGCT TATTGGTTTT CCATGTTTAG AAACAACCTA CAGGCAAGTT
 751 ATGACACTTG TTTACAGAA CAAGATGAAA ATATTATGAT TCTCAAATTG
 801 TAAAAGTATT TTATTAATA AAATAATTAG GAGTGTAGGA GAAGGAAGGA
 851 AAGAAAGAAA AAGTATGCTA ATGTCCTTAT TTTTATGGG TAACCAGTCT
 901 AAAATCAGTA AACCAAGTCA AAAAAGCTTT AGTGAATTAT TCAGATCTAG
 951 AATGGCTAAC TTTAAGTAAC AAGCTAAAA CAGAAACCGT CAATAGTGGT
 1001 TGCTGCTGGG AAGTGAGACT GGTACTGTGT GAAGAATGAG GAAAACCTTT
 1051 GTAATCATT AGTGAGTTTC TTTTTTTTTT CTTTACCCA TATGCATGTC
 1101 TTACTTCTAT TCTCTCTTAG CTTTAACTT GCTTCTTTTC ATCTTTTATG
 1151 TATATACATT TAGGCTGCCT TATATTAATA ATAGTTTCAT TTTTGTTCCT
 1201 CCTGCTTAAA AACTGTGTG CTATTTTTTT AAATTCTGAG AACTGCTTTC
 1251 TTTATTTCTA GACAATTCTC TGCCATTATC TCTTCTGTT TTGTCTCACC
 1301 CTAGTCTCAC AATTCTCTAT ATTGGAATGA CTATCAGTGT ATATTTGAAC
 1351 TTGTAATTCT TATTTTTTCC CCATTCCTCT TAACCTCTTA TTTGTATTTT
 1401 TCTTTTTTTA ATCTCTTCAT GCTATAATTT GAGTGATTTT CACAGATCTG
 1451 TCTTTCAATT TTATAAGTCT TCCTTCAGCT GAGTTTTTTT AAATTTCAAT
 1501 GATTCTATTT TTTTCTTTTT TTTAAGAATT CCTTTTTTTG ACTCTTTTTG
 1551 CAACAGCCTG TTCTCCTTTT ATATTCCTTT ATAATGTTTT TATTCTGTGA
 1601 AAGTTATTCT CTTATTTTGA ATGTTTTCTT TCAAAATGTC TTTCTTTTTA
 1651 TTAATTTAAT GTAAAAGTCC CTTTTAAATT GCTTTGTTAT TTGTAGTTCC
 1701 TTAGATGTGA ATTTTATCAT TTCTTGTCCT TACTGGCACT CTTGCTAGTG
 1751 AGTTTCCATG TGTGTTCTAT ATGTTTTGTA ATTTGAGGAT GTGAACTTTT
 1801 CTCAAGTGTG AGTTGCCTTT CAAAAAAGTA CTGCCATGGC ACTGGGTTGT
 1851 GGAGGTATTC CCATGTGGTA GTTCTGTTT GTCAGAGGAA TAGCACATTT
 1901 TGTGACTTCT GGAGCAATTT TTATGTTAGT TTCTCTGCTC AAGATTTTCT
 1951 TATCAAATGG GTATTGCACA TGTCATGACC ACATTTTCA AGAATGATAG
 2001 TGTTTCTCCT AATACGATGG TTCAACAATA ATTGAATGAA TCTAATGGTA
 2051 AGAATTTTCA AAGAAATTAT ATCAACTACA TATAGTAGAT TCAAGGCATT
 2101 TTTCAAAAAC ACAATGCCAG TCCACCCCTT TCACTATAC AATTGAGGAA
 2151 AATGAGGTCC CCAATGTGA AATGACTTCT GCTGAGATCC AATGAATTAA
 2201 AGGCAGAGCA GAGGCTAAAA TCTAGATCTC TTTGTTGTTA AAATACATTT
 2251 TAATTTGACA CAGATGATGA GTAATGCTGA CCCAGAGGTA AATCTGAACT
 2301 TTCTTTTGT ACTATTCTTA ACTTTGGCTT CAGGATCCAA GTGCCTAGAA
 2351 AGTTACTTCC TAAACTTGAT CCTCACCTAT GTTGCATATT ATCAAGCATT
 2401 TGGTGGTGT AATTCTTTCA TGTCCAATTA AATTAAAGCA GTAATTTTCT
 2451 TTCTAGTTAT TGCTAGTAGA GAACTGGTA GATTCTGCCT TGGTAGACCT
 2501 TCCTCTGCA ACAATTTACT TTTGTCTTCC TTTCTTTTAA AACATGTATC
 2551 CCCTCACAA ATACCTAAAT TTCCTTGAAG ACTGCTGCCA TGTTTTAAAG
 2601 TTTCTTTTTT TTTCCATAGT GACTAGTAAA ACCTGCCATT TTCATTATAC
 2651 ATAGGCACTC TATAAATATC TGCTAATTTA GCAATTATTA GTAATTTTCT

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FIGURE 3A



2701 TTCTTCTCTT CCATTTCTTC CTTTCTTGTA TTGGGTAAAG GAACATTTCA
2751 GGATTTGCTT ATGTAAAGTT TTCAGGAGTT TCTTTCCTTC CTCCCTTTTA
2801 CAGAGAGCAT ACAAAATGTA GATGATTCAT ATTCACATTAT TTCATTTAAA
2851 TAAAATTATA ATGATGTATG TTGTGTTCTG TTTGCAGAAC AGAGTGTTCT
2901 GAACATCAAC ACAAAGTGGA AGAACCTTAA GCTGAAGGTA CAGTATATTA
2951 TTTACTCTGA AGGGGCTTGT GTGTGGACAA GAAAGCGCTG ACAGCTCAAA
3001 TGGATCCCAT GGAAGTGAGA AATGTCAACA TCGAACCAGA TGATGAGAGC
3051 AGCAGTGGAG AAAGTGCTCC AGATAGCTAC ATCGGGATAG GAAATTCAGA
3101 AAAGGCAGCA ATGAGCAGGT ATGGGGTTAA AAATTACTAT GTTCCATGGA
3151 AAAATAAGAC AGGATGTGGA CATGGAAAAC AGGGTCTTGA TGGGAAGAAC
3201 TGGATTTATT ACAGGTAAAT TTGTGATAAC AATGATATTG ATGCTAGCAC
3251 ATCAATTCCC TGGTCTGAA ATACAGTGAT AATGTCAATC TCTTTTGTGA
3301 CTGATTTAGA ATTGAGGTTA CAATGTCTTT GTCTCCATTA ATAATGTGTA
3351 ATAATTTTAA TTATTTTAGC CTATTGCTCC TCTTATCTTT CTCAGATTCC
3401 TCTTTGAATG TTGCTACACC TCCTGGTTTC TGTAGGGATT CTTTTCTCTC
3451 TAAAAGTATC CTCTGGGCAA GCTCACTCAC AACTACTATG GCCTCACCTT
3501 CCAAATATAT GCCATATACC CAGCCTGTTA AGTTTCTCTA CTGAATTTCA
3551 GATAATTATA TCTGAATGTC TACTGCACGT CTCTACTGGA CCATTACTGT
3601 GTCTAAATTG CCTCATTTAT AAAGTTAAAC CTGTAATGTC TAATACTGAA
3651 CTCCTATCTT TCCCTCCAAA ACCTGCTCCT CCTCTAGTAA TCCCCATCCT
3701 AGTGAAAATC ACTGCTATCA TGTAGCAACT CACTCAAAAG CCCCTAGGTG
3751 TAAACTTTGA CCCACATAGC CAACGGTCAG TCATATCCAG TTGGTTTGAC
3801 CTTATTAATG CTTCAAATAC ACCTACTTTT CTGTACCCAT TCTACTGTGG
3851 TCTTACGTTA GGCCTACATT AAATGTGAGA CAGGGAGAGA GCCCTGATTT
3901 CTCTCCCTGT CTTACATTTT GCTCTCCTCT GTCTAGCCCT CTACACTCCT
3951 GCAAGAGCAA TCTCTTACAA TTGCAAATTG AATCAATTTT CATCCTTAGA
4001 TAAAGCCCTT CTGCACCTCT CCAATAGCCA TAAGAGAAAG TAGATTACAC
4051 ACACTGCTGG GCACGTAAGG TCCTTTGTGA TCTGTTCTTG ACCTGCCCTT
4101 CCTGTCTGT TTTTGGCCCT CTCCCTATTT GTTACTTGTT GCCTTCACTC
4151 ATTCTGCTCC AACTGCCTGG AATCAGTCAC CTGCTCCCCC TTTCTCCGTG
4201 TTGACACCTC TCATCCTTCA AGAATCAGCT CAACATCAGG TCTCCTATGC
4251 AGCCTTTTCC AAATTACTCT ACTCCCCCAT GTAGAAGTGA CTGCCCCTCC
4301 TTCATGTACC CTCTCCCTGT GCAGATGTTA ATTACGCCAC TACTACAGGT
4351 TAATGGCCTC TGTGGTCCCA CCACCTGCCA CATTGTCTGG TGCATAGTGA
4401 GTGACAATA GTTATTTGAT AAGTCAATTG ATTTCCCACA AAATGTTATA
4451 TCAAATTGTA CATGATTTAA GATGCTCAGA AGGGAATTTT TGACCAAAATC
4501 TAGGCGTGAA ATAGAGAATA TTGTGCTCAA ACAAAGACTT CTCATTTTAT
4551 TTACAACACC CAGGAAAATC CATCAGGAGA AACTACCGTT CTTCTTCAA
4601 GTAGCTCAGT GCAATGAACT TTAGGGATGT CGGACTAGAG AGGCCACTGA
4651 GATGTAAATT ATAGCATTTT CTAATTTAGG TGACCCTTGA AGAAACACTA
4701 GGGTGCTAGA AGACAGGGCT TTGGAGTCTG CAGAGTAGTT GCCTGACTTT
4751 AGAGAAGCTG TTTGTCCTCT TTGAGCTTCA ATGGAAAATG TAAAATGGCA
4801 AACCAACAGC TGCTTTTCAA GGATGAGATG GGTGACCAGA ATATAGATGA
4851 CATTCAATAC TTTTATTATA CTCTCCTTC ACTGCATTAC CCTCAGTAAA
4901 TTGATTCAAA CCTGAGGATG TTTCTGAAAG GCATGCACAC AAATATGAGC
4951 TCTGCCGAGG TTGACAGAGT TAAAGGGGAC ACCCTCCTAA GAACTGTCAT
5001 AGTGTCAATC CACTTGATCC TCAAAAGCCA GAGTAGAAAG AGCATGAATG
5051 CTTTTCTTAA GCTTCATGCA ATGTGTTCCG AACCCTCAC AGTGACTTAC
5101 CTTTTATCTC CTGGCTTAAA CATAGGACAT CATTTTGCAG TTTTAAAAAT
5151 CAGTTTAAAG AGATGGGTTT TATCTATGTG TGGTTTGGAT TGAACCCTTA
5201 AATGTAAATT TTTGAGAAAT TCAACATAAT GTATTTATTT GTGATCATT
5251 TACTTGTGTT TTCAATACAT GCTGGGTTTG GTATCAAAAC ATTTAACATA
5301 CTGGGGACAT TTCTCATCTA TTTTATACAA TCTTGGCATG TTAATGACT
5351 ACAACTCATC TCATGCCAAA ATAAGAACAT GCAAATGCCT CAAAGAAAGA

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FIGURE 3B



5401 AAATCTGTTT ACTTTCAAAT TCTCAATTTT AAAAACTACT ATGGAATACA
5451 GATTTTAGTT TATTGATTAA AATAAAGATT CCAGAGTTTA AATTCTAGGT
5501 GGCACTTTGT TTTTATAGT CCTCAGGCC ATTTTAGGCT TCATTTTATC
5551 CTGTCATCTC AGTCTCCAAC TGTGAACATT ATGTACCAGT CTTACATAG
5601 CAGGTACATT AATTACAGAC CATTAATGTA AACCACAAAA GAGTGGTGGG
5651 CAGTGGGTGG GGGGTGAATG GAAATGGAAA GAGGCAACAA CTGAGGGCAT
5701 TGTGCTTTCT GTGAGAAATA TGGGGAGAAG GCTAGGAAAT GTTCTTAACT
5751 TGTGACTCA GAGCTATTTA TGCCTTGAGT TCTAGAAAAG CACATACAAC
5801 TTTGTGGTTT CGTGTGCTGT TTCTATCTAC ATCTCATACT GTTTTCTATT
5851 CTCAAAAAGT AACCTGTCA TCCTCTTTCC TCTCCAGATT ATTTTCAGGA
5901 TTAGCTTCTG TTATAAAAA TAGCTTGTA AGATCTCCTA CAATAATTAT
5951 TTTCTATTTT ATTTCTAAGG TTTATTTATT TATTTATTGA GACAGACAGA
6001 GTTTCACCTC TGTGGCCCAT GCTGGAGTGC AATGGTGCAA TCTCGGCTCA
6051 CTGCAACCTC TGCCTCCCAG GTTCAAGCGA TTCTCCTGCT TCAGCCTCCT
6101 GAGTAGCTGG GATTACAGGC GCCTGCCACC ACACTCGGCT AACTTTTGT
6151 ATTTCTAGTA GAGACGAAGT TTCACCATGT TGGCCAGGCT GGTCTTGAAC
6201 TCCTGACCTC AAGTTATCCA CCCACCTCAG CCTCCCAAAG TGCTGGGATT
6251 ACAGGCGTGA GCCACTGTGC CTGGCCTCTA GGATTATATT AATAGAACAA
6301 TCTTCAATTA TTTTATCTTT CTTTATCTTT CTTTTCATGT AGGAAATGTC
6351 CTAAAATTTT CAAACCCTCA ATTTGAAAGC ACTTTTAAAA TCATACATAG
6401 TCGAGCATTT TATATAAAAA CAACTAAAAA GTCTGTGACA TTTTGCAGTA
6451 TAAAAATGCA ATGGCAGCAG CAGGCCTTAT TAATTGAGCC TCTTGGAAAT
6501 GTGGCTGGTC CTAGGTCCGT AGCCTCAAAG GCCCTGGCTT GTAACCTGCAG
6551 GAGCTGACCA GCACAGCTCT ATAACCAAGT TGTACATCTT CTAGCCTGTG
6601 TCCAAGAAAA CCAGAATCAC AACGCTCTGT GGATAGTGAC ATCTTAAAGT
6651 TTTCTTTCCC TCCCAACTCT TTTGCCAGTT CATTGAATTG CTTTAATAAT
6701 TTCCTTAGTT TCATTCATTA TCTGTTAATA ATCCATGTAC ATTTTGAGAG
6751 TAATTAANAAC ACATACGCAC ACACAGAAAC AACCAACACA ACACACAGCT
6801 ACCACTGAAT TACTTTCCAG TAAGAGATGT ATGTATAAAT GATTGTACCA
6851 AAAAAAAAAA AAGAAAGAAA ATACCAGCTA CAGGGCCCTG CCTGGGACTG
6901 CTTGATGCCA GGGGGAGAAT GGGGTCTCCC CCTGGGTATG GGTGGGTATG
6951 GGCCTGCTGC TTCACCTTTC TGAGCCACAG TTCCCTATAG GGATATTTTG
7001 AACATCAGAT GAGATAAGGA TCACAGTGCC TAGGCATTTA ATAAATATTC
7051 GTTGAATTAA TAAAATCATC TGATTATGGT ATGGTAGTAG TTCAGAAAAT
7101 TCTGTCATAA CCCTGTACTC TTTCTTTGGA AGGGCTCTAA ATGGGAACAC
7151 AATTAGTTGT AGTCTCTTGC ATAGCTAATG TGAGAAAGAG GGAATGTGGT
7201 ATAAACAATT TTTTAACTAA AAATAATATT TCCTTCCTTT ATAACATCCT
7251 TCTTCCATCC CAAAGTATAG TTGTAATGG AACTCAAAT TGTTGGTCTG
7301 GAATGACCGT TAGTGTGAAG GAGGAAAAGA AAATTGGGGT GTCTTATTTT
7351 CCCTCCTCTG ATTCAGTTAC TTAGATCACC TGAAACATAC ATATGATTCA
7401 GAGCATATAT TTAGATGTTT TCACTTTCTT ATTTGTGTGT GTGTGTGTTC
7451 AGTCAATTTG CTAATGAAGA CACTGAAAGT CAGAAATTCC TGACAAATGG
7501 ATTTTTGGGG AAAAAGAAGC TGGCAGATTA TGCTGATGAA CACGTAAGTG
7551 AATCTATGCT TTCAGGCAAT AAACGGGACT GAGGGTGTCT GATCTACCTA
7601 GGTCTCTGTG GGAAAACAAT GTGACTGAAA TTTTCCAAGC CTTGATCAGC
7651 ACATTCTGTG TTTATTGAGG CTCTTACTGG AATAAGGGCT TGTTTTTTCC
7701 TGTTCCGCAT ATGGCTGCAT GAATCATTTA TGAAACTTAT GTGTTTTGGG
7751 GGGAAATCAT TCTAACCCAA AGGTAATCTA CAATCATACA TGTTCCTT
7801 TCTTTATGTG ACTCCCCTTG TAATTTGTAT TTTTACTGAG GCCTCTGCTG
7851 AAACCAAGCA CTGCATTCCG TTGAAAATTA CATGCTTTTA TTGATGTTGA
7901 GTAATGGCTT TACTCCTGTA ATGTTATCTT AGTCTTCAAT TTTGGACTGT
7951 AATCTGCAGA TAATGTGAGA ATAAGGATAA CCCCTAAAGG TATGCCCTTT
8001 GGCAAATGTT TGCTTATAAT ACATCCCTTC TTTTCAAGC ATCCCGGAAC
8051 CACTTCCTTT GGAATGTCTT CATTTAACCT GAGTAATGCC ATCATGGGCA

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FIGURE 3C



8101 GTGGGATCCT GGGCTTGTCC TATGCCATGG CCAACACAGG GATCATACTT
8151 TTTATGTAAG TGAATGTATA TGTCTACATT TGGTGATGAA GTCCATGCAT
8201 ACCTGGTGGC TTTTTC AATT AACAACTCTCA AGTTTGATCT TTGTGAACGT
8251 GAAGACTCAG AGGAGGCTAA TCATGGCACT TGGTCACCCA ACCATCCCTA
8301 ACCCAACGGC AGAAAGTGTA TGTGCTCAAT CAACCAAAGT GCTGGAGCAG
8351 CCTCGCCAGA AGAATTTTGT TATTCAGTAA ATACTTGAAA TAATTTGGTG
8401 TTTAGCAACC AAAAAAGATCT TTCCAGAAAG CAAATCTGAT TTTATCTCAT
8451 TCTTAGGAAA GAAGCAACCA AGCCTAAGAG CCCTGCATGC CCTTGCCTAC
8501 CTTATGTCCC ATTCCCTGTA CCCCTGTGCG ACAGATACAC TGGGCACAAT
8551 AGCCTTCTCT CCATCCTATG AAGATGCCAC ATTCCCTCTC ACCATTGGAC
8601 CTTTGACAT GGTCTTGAA CCCTCTTCTC TTCCTTCTTC ATCTAGTTAA
8651 CTCCTCATAT GTCAGTTCAG TCTCACCTGA ATACTGCGCG CCCTGATCTC
8701 CATGACTGGG GCAAATCACC TTATCATAAC ACTCACCACA ATTTTAATGT
8751 TTTAGTGCCA TTTGTCTGAT TCATTTGGTT AATATCTGTC CCTCTTGCTG
8801 GACTATAAGC TCTAGAAAGT TGAGCCCATG TCTGTTTTTA CTCACCAATG
8851 TCTCTACCTC CAAACCTAGA GCAGTGCCTG GTACAGGCAA TATTTGTTGA
8901 GTGACCAAAC CTTATTCTTA AACCTACGTA CTTTCACCAA ACTTGTTCAA
8951 ATGCTGCCTA AGGGTAGCAG CATCTGGTAG TTGACCTGTA GGGTGGATAC
9001 TGCAGTGTCT ATGACAGACA ACAACAGACG TTTATGTGCA TCATGTACAG
9051 CCTGGCATT TCCAGGATAT AGTTGGCAGC AGTGAATTC TTCACAAGAA
9101 TAAAGTCTGA TGTTAGGCAC CACTGTGGAC ACAGATCCTA ATCCCAAATG
9151 CAACGCTAGA GAGTTAAATA ACTGTCTAAG AATGCAACAT TTATATCACA
9201 AATATGTGCT GTTTATGTTC TGAATATCAC ATATGATTAG TAATCACACA
9251 GCTATTTGAG GGCTAAGCAT CAGGACTATA AATATTTGTA TTGTGTTAGT
9301 GCTTTGATTG AACTCTTTTA TGTATAATAT TCTTCAGCTG AATGGGTTTT
9351 TATATCAACT TTACTTTTAT ATAAGCCATG TTTTGAAATA AACTAGGATT
9401 TTAATAATCT GAATTTTAAT AGCTATGTAT GTAGTCATAT ATTTGTATGC
9451 TTTTGTAATG TGCTTACCTC TAAGACAAAA AAACCTGCCT TTCCTTATTA
9501 ATTATACATA CCATTAAAAT GAATTAGGAA GTTACAGATC ACTGATGAAT
9551 AGAAATAGGA AAAACTTCCC CCAATCCCAC AGTCATAGAT CATCTTCATG
9601 AGAGAAGAAT GTTCCACTTT TTAATAATGAG GGCCTCATT TAGGCTTATA
9651 AACACTTAGC AGATGAATTT GGTGAGAACA ATTAAATCAC TAAACATCAT
9701 GGGGTGTGTT TTGTGTGTCT AAGTAGCCCA GACTGGATTA AGCTTTCTCT
9751 CTTAATTTAT AGCAAGTGAC ACAGTATTTT AAAGGTTTTA CTCTTAGTAT
9801 TTTCTGCCAG AGAAAGTACA TGTTTAGAAT ACAGGGAATG CTCATTATTT
9851 TTCCAGGGAA CAAAATTATA TAATCTGAAT TACATTATTC CTTAAAAACA
9901 GTTAAGTTCA TAAGGCATAT GGAATAATAT AGGAATAAGT CATTGGTTAG
9951 ACAGTTCTGG CAAACATACT CTATGGAAAA TAAGAGTGCA ACATAGCTAC
10001 AGGGGTTATA AAATTTATAA TTCATGGTCC AAATGTACAT TTGTAGTATT
10051 GATTTTCATTG GGAATTACCA AGGGATTAGA TCAATTGTGG GGAAAGTGTA
10101 TTTTTTAAAA ATAAACAAAG ATAAAGATTT TTTTCTGAA TTCCAGGTAA
10151 AAGGCAGCAT TGCTCCTCCA TTTATTACGT AGATGCTTCT ATCAACATTC
10201 TTATTTTTGT GCTCCAAATC TTGGATTTGG AAAAATACCA ATCCGTATAA
10251 ACATAAAGAA ACCATACATG CATGTGGGGA TCCTAACACC AGAAATGACT
10301 CTGAATGCAA AAAAAAAAAA AAAAAAAAAA GGAATTTTC GTGCCCCATC
10351 CTTAGCTTTC TCTGCTTCT CTATTATATA TGCAACTGCC TGCCCCCTA
10401 TCTTACAAAG TACTTCGTAA TCTAATGCAC AGGATCAGCA GTAATGCAGC
10451 TCAGACTGCA TGCTTTCGCC TTTGGATTCC TAGATTTTCAG ATTAAGGTTT
10501 AGTCAGGCTA TTGAATAGCC CTTCAATTCT AAGTGCTGAT GTGAATATCA
10551 TGCAAATATG ATGTACATAT TCCCATGTGC TGAGTAAGTA GATGTAGCAT
10601 TTGCTAATGT TGCTATACAT TTAGCATCTA AGTTATGAAC CAGATTCTAC
10651 CACTGGGTAA CATTAAAAAA AAGTTAGGGA CTTGAGGTAT GTAAAAATA
10701 GCAAATTCTA TTTCTACGAC TTTAAAGGGT ATGTGTAGAG TTCTGAAAAG
10751 AATTTCTCAG CCTCCCCCAA ATCCACATAC TTTTGAAAG CTGATGATTG

FIGURE 3D

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10801	AAAAGATTAA	TGTGATCCTT	TATTGTAACA	TCTAACATAA	TTACATTTTA
10851	TTTATTGTAG	AAACTTTTATT	ACCTACTCTC	TCTTCCCTTT	GCAGAATCAT
10901	GCTGCTTGCT	GTGGCAATAT	TATCACTGTA	TTCAAGTTCAC	CTTTTATTAA
10951	AAACAGCCAA	GGAAGGAGGT	ATGCTACCAC	TTGAGTCCAA	CACATTCTAT
11001	TTTAATTCTC	ATAAAAGAGT	ATTTCACTCT	GTTGCTTCAT	AACCTTAGGA
11051	TGATTATAGT	CAGTTTCACA	TTTCATTTTC	TTCTGAGCCC	AGTGACACGA
11101	TCTCTCAGTG	TTTATAGTTG	TTTGGGCAAG	TGAGAGGCAG	GAGTGAAAGT
11151	CAACTGGCTC	AGGTTCAAGA	CAAATAGAAA	AAAGAAATTT	CTGATATATG
11201	ATAGAAATAA	CTGTTTTGAC	TTGCTACATG	CAGCTAAAAT	AAATAAAACC
11251	ATTGATTCTT	GTTTGGAGAA	CATTTTGATA	TATTGCTTAT	TGGTTTTTGA
11301	GGTTGCATCT	TTTGGGCTTA	TAATTTCTAT	ATGATGTTTA	TTTACATGTT
11351	TGAGACTCCA	GCATGGAATT	ATATGACAAA	AATATTTTAG	TCATTAAAAC
11401	AATCTCTTTA	ACAAGGCTAT	TTTATCTTTG	ATTGTAGGGT	CTTTGATTTA
11451	TGAAAAATTA	GGAGAAAAGG	CATTTGGATG	GCCGGGAAAA	ATTGGAGCTT
11501	TTGTTTCCAT	TACAATGCAG	AACATTGGAG	GTAAGGGGAT	ATACTTTCCA
11551	ATGGATCCCA	TAAACTTTCT	ATAGCGTGTT	CAATAAATAA	GAAAACTTAT
11601	GGCAATAAAC	AGGCACTTTA	GATACAGAAA	AATTGCTACT	TATAGTTCTT
11651	AAATTTTAAA	ATGATAGTTT	CTTAAATAGG	TTTGTGTCCT	GCTTTAATTA
11701	AAAACAGCAA	TATCTAAGAA	TGAAAATAACA	TATAAAACCC	TGCCAATTGA
11751	ATTCTAGAAT	TAAAATATAA	AATAAAAAGCT	TTCTTGATTT	TTAATGTTAT
11801	TATAGCATGA	ATTATTACTC	TTAAAAATTG	AAGAATTTGT	GCTTATATCT
11851	GTCATTGACA	AAACAGTTGA	CGTTTTCTAT	GTGTGACTGA	GTTTCGATTTA
11901	CTAAACTGAA	AAGTGGGTGT	CTGGGGGAAC	ATAGCCAAAT	GCTGTGGTCC
11951	TTGAAACGCA	GCCTGCACTG	AGCCAGCCCA	CTAGACAGTG	TCTCTGGAAG
12001	TTTACTAAGG	CAAAAGTCTG	GCTAGGCATC	AAATGCACTA	TAAACCCCGG
12051	TTTGTTGATT	CTATGGATTG	TTATAATTCC	CACTGAATTA	TCATTTCCAG
12101	TGTAGGACCT	AGAAATATAT	ATATATATTT	TTAACAATGT	TCTCTCGTTG
12151	GTGTGTTTGC	CCACCAGCTT	CATACTGTTT	CTGTTGTGTC	TTTGGCCCTC
12201	AGAAGGCATC	CAAACCCATA	TTTCAGATGT	CCTGCCGGCT	GCTTCCTGGC
12251	ACATGGCCCC	AGCCATCTCC	CCACATAATG	ACACTTACTC	CCTCACCTCC
12301	TACCCAGTCC	CTAAACCTGC	TATTCTATTT	CTCTGATCTT	TCTTTTCTCA
12351	GTGAATACCA	CCAGCAGTCA	TCCAGTTTCT	GAGGGCAGAA	ATCTGGATGT
12401	CAGCGTAAAT	GTTTCCTTTT	CCCCAACTCT	GCATGTCCAA	TCAAATGGCA
12451	AAGTCTGTTT	ATTTGATCTC	TTACTTATCT	CTTGAACCTC	TCCTCTCTGT
12501	CCGTCCTCAT	GACCACAGAT	GATCACCATT	TATAGCTCAG	ACTATTGCAG
12551	TAGTCTTCTA	ACTGGTCTTC	CTGGCTTGAG	TTTCCCCTGC	TCTCAGATAA
12601	ACTCTAATTT	GTTCTCCAGA	TAAACTTTCT	CAAATTTGAG	TCTGTTTCTA
12651	CTTTTGTCGT	GCATAAAATT	CTTCAGCATG	CCTTTATTAT	TTTCAAGGAA
12701	AAACTTAAAC	TCATTGGACT	GACACAAGAT	CTTCGTCTAG	TTCTTCTGCT
12751	CAATCTTTCT	AAACTTTTCT	AGCAATGCCC	ATATCTATCT	ATCTTTATCT
12801	ATCTATCTAT	CTATCTATCT	ATCTATCTAT	CTATCTATCT	ATCATCTATC
12851	AATTTATCCA	TCATCTATAC	CCTACATGTC	CTGTGTCAA	CCATAACAAA
12901	TTATATTTAT	TCCCCTAACA	GTAATTTTTT	AATATTTTAA	AAAATCATCC
12951	ATGCCTTCTT	TTCAAGGCT	ACTTTCTCCC	CTTGACTGTC	TCTCAAAGTC
13001	CTCCAACCCT	AACACACACG	CACACACACA	CACACACACA	CACACACACA
13051	CACACACATT	TTCTCTCTCA	CTCTGCTCAC	CTGGTCTATT	GCTCCTCTAG
13101	ACTGGTAAAT	ACTAGTTTCT	CTGGGCTCTC	ATGGTCCTGT	TTGTATCTAG
13151	TATGTTACTG	TTTTCTAAAG	GATATTTTAA	AACACTTGAG	TAGAGAATAA
13201	GCTTTTGGAG	TCTGATGGAC	CTGAATTTGA	GTCTGTTTCT	GTCATATCT
13251	GTGAACTTGG	GAAGATCACT	GTAATCCTTT	GTCTGATTTT	TTTATGTATA
13301	AAAATTACCT	TACAAAGGCT	ATTGTGAGGA	TGAAATAAGG	TAACATATGG
13351	CACATAATAA	GTGTTCTGTA	TATGCTTCTC	TCCTCCCTGG	TTCTCTGCTT
13401	CCATATCCAT	GTCTCTGGAG	TTGCCTGAAT	TATTTTTTAA	ATAGGCATTT
13451	AAAAAATTAT	AAAACAAATA	TATGATGATT	GTGAAAAACT	AAAACACTGC

FIGURE 3E

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13501 ATAAATATAT AAATTACCAA GAAAAGTTTA TGTCAGTCAT CCTCAGAAAT
13551 AACTACTCAT AGGTTTTCCC CTATGCCTAA TTCAACAAAT ACATTGAATA
13601 TTGTTAGTAT TGGATCATCT TATGATACCG ATTTTCAGCT TTCTTTTTAA
13651 ATTTAACAAT ATGCCTTGAA TATATTTGCA TGTTATTCTT TTTAATGATT
13701 TTTGAGGTTT CCATTACACA AATGTGCCAT AATTTGTTTA CAGTATCCTT
13751 ATTGATGAAC AGTTGGATTG TTTCTAATTT TTTACTGTTA TAAAAATGCT
13801 ACAGTAAATA CACTTGCACA GAGATCTTGC AAACAGGCAA CCCATTTTAA
13851 TAAATAAATT CACTGGAGTT ATCAAGGATT TCTGGAATGC AGAAATTTCT
13901 TTAGTAATCT ATCTAACTAT ACTCACCTG ATAATGGATA GTTGGTAAGC
13951 AGATAAGTAA AATTCAGCCA TATCTTATGA TTTGTGTTAA AAAAATTTTT
14001 ATATGTTAAG ACTACAATCT TGGGTAGAAT TTGACAGTAA TATCAAAATT
14051 GTCTCATTCA TTTTACTGGT TTGGAGCCAT ATGCATATTA GCCCCCCAAA
14101 TCCCAACAAA TAGACCACTT TACATTTGTT TCAAACCTCTC AGCCTTATCA
14151 AGGTTTAAAG TATCGAGCAT TTCATAGGAT TGCCTTATAG TTGGTCTAAT
14201 TTAACAACCTG AAATAACCAG GCATAAGCAT AATTAACCCT GGACTCAAGA
14251 AGTTGAGTGG CAGCACCTCA GCTGTGGTTC AAAGCATAGC CACTACTACG
14301 CTTCTAAACA ATGGAATAAA GTATAAAGCG GTCTCTCAGT CAAGCCTCAC
14351 ACAGGTAAGA GCGTGACTT TAAGGGAGTA AGATGAAATA TCGTAACATC
14401 ACCCCAGAAA TAATGCTCTC ACTTTGGTTA CTTTATTTGA TTAGTTGATA
14451 TTTGGCATAA GAGAAATCAC TTGTATTTCT CTATTTAACA ACTCTACATT
14501 TAGAACACTT AATTTTCTCA ATCCCCTAAA AAATTAACAT TTAGTGCAGA
14551 TGTTTTTACA TTAACAGATT AATGTCTGGA TCATTCTGAA TTTTTGAAGA
14601 CCAAACATGT TAACATCACT GACATCACTG AAAACCAGCA ATTAATAGCT
14651 GTAACATTGA ATGGTACCTC ACCAAGCCAG CTAATCAGAA ATATCTCCTG
14701 TGTTCACTCT CTGTAAGATT TAGCTTTAGC CAAGGTCTTT GCAAAGATTA
14751 ACCAAATAAT GTGTACAGAA GGTACATCCG CTATTGTAAA AATCATTTC A
14801 CTTTGACAGT ACAGAAGAAG CACCAGCCCT TCTGTTTTAG ATGTAGTCCG
14851 TCCTTTTCAA GCTGTATGAT TGTGGACATG TCAACTTAAC ATCTCGGAGT
14901 TTTTATATCT TCATCAGTGG AATGAGAATA ACAACATATA TCTTGTCA TC
14951 TCACAGGGTT TTTTATATCT TCAAAATGAAG TAATGTGCAG AACTAACCAA
15001 TGTGGGGAAT TATTATCATC ACTGTTACTT TCATATGAAG TGAAGAAAAT
15051 ATTTTTTAAAC TCAGTAGTTT AATTTACAAT TTAAGTATGT GTTTTTAAAGT
15101 GCCTGTTAGC AAAAATTAC TAGAAGGATG TAGGACACAC TTAAAGTTTT
15151 CATGTAAAT TTGTGAGTTC TATTTTTAAC TGAATCTTTT GGCCATGTGT
15201 CAACAAATTA ACGTTATCCT TCACCAAATG GGTGGGCTTG AAAAAGGCGT
15251 GATGCATAAA TATTTACAGT TGTAGGCAAA ATTGTAATGT TATGTATATG
15301 AATACATATT CATTTTTTCA GGGAGAAGGC TTGTAGATT CATCAAGAAA
15351 TCTTTCACAA GAGTAGATAA TCATTATGT ATCACTTACC TAGATGCTCA
15401 TGAAATTTTG CCACTTTATA TAATTCCTTA GTTAGCCAAA AGGAGAGTAA
15451 GATGAAGAGG GGGGAAAAA AAAACTTCTT TGACAAAGAT GGAGAGAAGC
15501 TGTCATCTCT TGTATTCTTT TATCAATCCA GGAAGCCTTT GGTTTTGACA
15551 ATAAGTGGTC TGAGACTTTG TGTAATCCTC AGATAGGTCC CGGAGGACTA
15601 GATTGGTGCC CATCTGCAGA AAACCAGAGG GGATATATTG ACTCTGCAGA
15651 TCTGCCCTTT GATTCTGCCA TCTCTCAGCT GGCCCATGCC TTTTGTGTC
15701 AGACTACTGC CCAAGTTATA GACACTAACA CAGGCACACT GAGTATGGGC
15751 TATGTTGATT TATAACTAAT GAGGGCAGAA CCTTAGAACT GCAGCTTCAC
15801 TGTAACCTTT GGAGCAGGAT TTAACACAGA ATCAGCCCTG ATACTGTTAA
15851 CAAAGGTCCA CCTGAAAGAG CTGGAAGGTC AAATGTCTAT CTTGGAAGAG
15901 AACTTGGAAG CAGTGCCAAA TACACAATGA CTTTTTTTTT CATTTGGGGG
15951 ATTAGATGTT CATCTTACAT ATCCCAAATG TCATAACTTG CTTGCATGTG
16001 ACTTCAGTAC TGTCCACACC ATTAAGCTGT CACATTTTCC ATTTTAGCAA
16051 TGTCAAGCTA CCTCTTTATC ATTAATATAT AACTACCTGA AGTAATCAGA
16101 GCATTATGAG GACTTGAAGA AAATACTGGG TATGTCTTAT GCTCCCTCTG
16151 TGACATCAAG TGACTCATTC TACTTGGTCT TTTCTGATT TAATATCCCT

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FIGURE 3F



16201 GTCTCTCACT TCTAGAGAAT GGTACCTCAA TGGCAACTAC CTCATCATAT
16251 TTGTGTCTGT TGGAAATTATT CTTCCACTTT CGCTCCTTAA AAATTTAGGT
16301 AAAGATATTT TCTAACTGGA AATATTTTTTA TTTTATTTC ACATTTAAAT
16351 AGGTTAGCTA ATTGTAGATG CCATATTCAC CTTCCAAAAT GCTTCTTCTA
16401 ACTTCTAGGT TATCTTGGCT ATACCAGTGG ATTTTCTCTT ACCTGCATGG
16451 TGTTTTTTGT TAGTGTGGTA AGTGATGTGA TGACATGATC CTTGCAGGTT
16501 GGTTAGCATG AGTTTTTTTG TGCCTAAATT AGTGTCTCA TTTTGTTCAA
16551 GCACTTCACT AATATGAAAT AGTTCTTGTA TCACAAGTGA TTTTCTTGTA
16601 GACTAATTTA GAGCAAAAAA AGAGCAGCTA CGATTTAAAG ATAGTTGAGG
16651 TAGAATATCA AAGCTACTAC TAATGGTTTG GTCTAGGCAC ACTGGTTATA
16701 TATGGGAAA AAAGGAAAAC TTCAAGCAGG AACATGACAA TAATCTGGCA
16751 TTTAGAACAG CAGAGGAGAG TCCCAGATGA GAAACAAGAA GGCTATATCC
16801 ATATTCACAT GAATCAGCCA TTCTCTCTTA CACATTCCAC CCATTAAGAG
16851 AGGACAAGAA CAGTGGGATT AAAGAAGAAA TCCTCCTCTC TAGGCCCTG
16901 ACAAAGAGG GAATTTCTTG CACTATCATG AATGCCAAAA TTTATAAAGC
16951 ATTTCCCAA AGAGGTAAAG GAGAAGGAAA AAAAGTTTGT AAGACCCATG
17001 TCACCTTAGT TTGAAGAAAT AAGGAAATGA TCATCTTCT CATGGAAGGG
17051 CATGAAAGAG GGTGGGAAGG ATTCTTGCAA AATATTGTCC TGTTAACTCT
17101 AAGAGGCAGG GCTGCCAATC ACAGCTCCAA CTCTTCCCTT AGAACAGAGG
17151 CTAGAGGAAG TTTACTTTGT CCATTAGTCT AAAAGGAATC CCTAACTGAG
17201 TTCCCTCACC CCCCACCCTA TAAGCCACAC ATATGGATT CTTATTTTATT
17251 GTTTTTTCTC AAAAAGCTGA TTTTTTTTTT TTTTTTAATG ACTGAGTCTA
17301 GGTGATTTAC AAGAAATTCC AAATACCCTG CCCTCTACCT GTTTTGATC
17351 ACAGTGTTGG AAATCTGTCA TTCAACAACA CGCTTCCAAT GCATGTGGTA
17401 ATGTTACCCA ACAACTCTGA GAGTTCTGAT GTGAACCTCA TGATGGATTA
17451 CACCCACCGC AATCCTGCAG GGCTGGATGA GAACCAGGCC AAGGGCTCTC
17501 TTCATGACAG TGGAGTAGAA TATGAAGCTC ATAGTGATGA CAAGTGTA
17551 CCCAAATACT TTGTATTCAA CTCCCGGTA AGTGAGCGGT CCGGGCTTCT
17601 AATGAGTACA GTTATGTGTT TTCTAAGTTT TTATTCAATA AACTGAGATG
17651 GCCTGAGATC ACCATCTATG TTGGAATGCT AAACACGTGG TGTGTCTTT
17701 GTTTTTTCTC CGGCCTATGC AATTCCTATC CTAGTATTTG CTTTTGTATG
17751 CCACCCTGAG GTCCTTCCCA TCTACAGTGA ACTTAAAGAG TAAGGCAGCC
17801 ATCATTTTAG CATTCTAATT TGCTTTGAAA TTCTGCTCAT ATGTTCAAAG
17851 ATTCTTTAAC AGGAAACACA GTTTATAGCT TCCTCTTCAG AGAAAAATATG
17901 TACTCCATCC ACTCCTCAGT AACATGCTTT AATCAGAAAG GTGGGAATCA
17951 GCCCACCACA GCACTACCTT ATCTTCTTTC TCTCCTTCT CTCCACCATA
18001 ATGGTTCAGG GGAGGGGTTT ATGGCAGGTG GACAAGGAGT CGATGGTTGT
18051 AATAATTTTG GCAGGTGTTG GGAATTTAAA TTTGAATTT GTTCGGAAGA
18101 AATGATGTCA GCTGGACTAG AAATGAAAAC ACCCATGACG ACCAAAACTT
18151 ATGGTTAGGG GCAGCCTCGA TAAGCCAGTG ATGTCATTTA TAGTCAGCAC
18201 CTAACCCTTG TCTAGAACAC ATTCATTACA AGAGATGTGT CAATATCTGT
18251 CCTTTGTTGT CTTATTTGTA CAATAGAGTC ACTGGCTAGA AAATCTTGTT
18301 TCTTCAGCT GATGGTCTAT GGTTCATTTG TATCTTTTC CCTTTGAAGT
18351 TGTTGATATT TGCTTGGGAA CAAAGGATAT GAACTCATT TAGCTGTTTT
18401 CCTCTTCTT TTAAGGGAGG ATATTATATA ATAATTCTCA ACTTCTTTAA
18451 TCTAGACATC AGTAACCTCA GTCTTCATTC TACTAAATA GCAAACTTT
18501 CCCATAAAT TCTGATTTAC CTCATAAAAA ATTTCAGAAC ACTTTCAAGT
18551 ATTTTGATGT CTTTGATTTA CTTTGAAAAT TACATGTAGC AGTTACTCCA
18601 GAAGCCTGAC AATTGATCTT TGGCAGCCAG GTTCCTTCTA GAATGGTTTT
18651 CAGAAGCTTT TCAGGTAGTC TGGACTCCTG GCAGTAGTAC TTTGCTGACT
18701 CTAAGGTTT CTTTTCTCA TTTAAAGTCA TCTCATTATG AAATGCAAAA
18751 GCTTTCTATG TTAGGAGCCT GTTTCATCTT TATGTTAATT ATATTCTTAT
18801 TCAGTGGGCA AGCTTACTGA CCTACGTGAA ATAGACTGTT CCTCTTCTAG
18851 GGAAATGATT GTTTTTAAGA CTGAAGGACT AGTGTTTAAG AAAAATGGAA

FIGURE 3G

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18901 ATGAATCCTC ATTAGCTCTC TAAGACAAAT TTAAATCAGC TATAAGTTTA
18951 TGTACTAAAT ATGTCTTCAT GATTAGCAAT ATAGATATAC TTTTTTATTA
19001 TTATTTTCAT TTTGAAAAGT GATTTTTTTT TGTAAGTTTA AAAAACAAAG
19051 CTTGGTGTTT TTTCTTTTTT CAGTCGGTCC CGGAGAAAAA TGCAAAACGGT
19101 GTCAAATATT TCCATCACGG GGATGCTTGT CATGTACCTG CTTGCCGCCC
19151 TCTTTGGTTA CCTAACCTTC TATGGTAGGT CACTCTGAAA GTCATTCTCT
19201 ATATGCAAAT CCTTGTTAGG CTGGTCCTTG ACCTGGGTAG GTATGATTTT
19251 TAAAAATTGC CTTCTATAAG CATGCTCTAT AGATGACACA TATTCAATTA
19301 ATATACTATT TTAGTTTTGT CACTTGACCT GAGGAAATGG GGCCTGATTC
19351 AGCCTGGCTA ACAAGTTACA AGAATTTGTG AATTAACACC TATTTTATAA
19401 AAAATATCCC TCAAACAAAA TTATTTTCCT CTAGGGATAG ATGATATTTT
19451 TCTGGCTAGA CTCCATAGTC CAACTCAGGC TACAAGTGAT GAGAATGAAT
19501 CCACTTGCAT GTGATAAAGC TCCTTTGATG GAATTATTA CTGCCACACA
19551 AATAGCAGGG AAAGTCCAG GTCCTCAAGT TTGAATTTGC CTCCTCTTTA
19601 CCACTCAAGT CAAATCTGGG AGCTTGGGAC TTTAGGTAAA ATTTCTGACA
19651 TATCCCATTC TATTTTGTTA TACTAAATGA TTTCTAAGA AAGAGGACAT
19701 GACAGAATTT CCTTCAATCT AAGAATGCAC CACCAAAAAA AAGTGACTAT
19751 GGCCACATTA GATTATGCCT GCAACATTTT CTCTCTGGCA TCTTAACAGT
19801 TCACAAAGGG AGTAGGATTG TACTCCTTCC ATGAAGTGTG GCCACATAAA
19851 CAGATTTTAT GGAATCACAT ATTGACCTGG TAGCATATGT TTACATGAAT
19901 CAGTGTATCA ATATAAATAT ATTTTGTAT AAACCTCCTT TTAAAGTTTT
19951 TAACTTAATT TTTTCTTAC TGACTTGGTA AATTGAATTG CATGTATGAC
20001 AAATTGTGGA GGAAAAGATT CAGGAGTAGG CCACCATTGT CTTAGGTTTT
20051 TTTTCTATTT GACTAATATT TGACTATTAA CCAAACATGT GCTTTAGATT
20101 GGGCATTAACT TTTTGGCCGG TTGTGAAATA ATGAATGACG AGGTCAATAC
20151 TACTGAAGGT ATTTTCACTA CTTTTTGTCT GATCTTGAGG TGAAAATCCA
20201 ACTACGCTTG ATTCCATAGA TATTTTCTTG TTATTTGTGC TTGGAGTCCT
20251 GAATGAAGGT GTTTTCAAGT AGGGCTGCAT CTTCGTCTTA GAGTAGTACC
20301 CACTGGGAGA CCATCTAAAA ATTATACTAA TTTATCCCTG CACGTTACTT
20351 ATACTTATTT TAATGAGTTT CATAAGACAA GCAAAAACTT GAAAGAGCCC
20401 AAAAAATATCT GTTTTAGTGT GGTGATGGAG TCATAGTTGT TGAGCTTGAA
20451 AAAATGGTAG CAATCATTCA TCCTAGAGTT TACACACTGG GTTTGTAACC
20501 TGCATCAGGA GTGGCTGCAC AGGTAGGGAC AGGGGAGGTG GTAGGCTGGG
20551 AGAGACAATA TGTGGGGCTT GGGTCTCTCA TCCCCTTCAA CAAGAGCACC
20601 TTGGTCTCTG TCTGATTTGT AATTGCTTCT GTACAGCGGA GATAGATTTA
20651 TCACAATGTA AATGAGCTTG AGAGGCTCTT TATTTTGTAT TATACCTTCT
20701 GCAACGTTAT CAGCTTCAGG ACCTCTTTGT TCATTTGAAT GAAGGTTGCA
20751 TAGCTAATGA GCTCAGAGGC AAGACCAGAG GTGCCTGGAT TCCCAGGCCT
20801 AGGTCTTTTC CTCTGTTCTG TGTTCTCTCT ATAAAATGTT GCCATAAGTG
20851 ACCTGTGCTG ATTTGACAAC ACCAAGCGGT TTCACTTCTT TTTTCTGTT
20901 GTAGGAGAAG TTGAAGATGA ATTACTTCAT GCCTACAGCA AAGTGATATC
20951 ATTAGACATC CCTCTTCTCA TGGTTCGCCT GGCAGTCCTT GTGGCAGTAA
21001 CACTAACTGT GCCCATTGTC CTCTTCCCAG TAAGTACATA AGACTTTGAT
21051 GAAAGAAACC TACTTGACCC CATAAATTAG TACATGTGTT CTACCTTCAT
21101 TTTGATTTAA TTATAGGGTG AGTTTGCAAT TGCAATGCCT GAGGATATTA
21151 TTTTCTATA GCATTTTGAG TCACTTAAAA TTGGCCATTT AATGTGTAGA
21201 TAGAGCAAGT AGTTTCAGGT GGTATTTTTA TAGTGTAGGA AAAAAATCAT
21251 AAAACTTATT TTTAACTCA AAGTTGAAAA GTGGAGCTGG AGCTTCTGTC
21301 TTGTGGATTA GTAAAACCTGA GTAGGAGTTC ATATAACTTT GGAACCTTGA
21351 AAGCCAAAAC CATATTAACCT TTCAAATCTT ATTAATTTTC ATCAGATTTT
21401 TGAAGGCATT TCATTTTTTT TCCAGTTTGT TGTGCTGCAA TAATATACAA
21451 AAGTTGCCTT TTTTAACCTG ATGCCTTGAA GGCTAATGAA AAGGGGATTC
21501 ATGTTAAGTA AATTATATAC CAGAAAAAAA TTTTTCAAAA AACAGTTATG
21551 CTATCTATCA CATATCTCTC TCACACATGG CCTCTGCCAG ACTCACACCA

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FIGURE 3H



21601 GGTACCCCT CCCTGGCATT TGTCATTGGT GTCAGTTTGT TCTGAGATCC
21651 CAGAGCAGAG CTGGTAGTGA AGATTTGGGC TGTGTGAGTT AAAACCACCA
21701 CCTAAGGATA AACACAGGTC TTCACCCTCC TGCCAGCTCC TGTTCATATA
21751 ACACTGAATT TACTCATTCA TTTGAGGGGG AAAAAAATAA GTGACACAGT
21801 AACCAGCACT GTCCTGGACA TAATGTTCCA TACAGGGCTG GCATATGAAG
21851 ACTATTTCTA TAATGACACT GTGGTCACTT TAAATGCAGC TTGTGTGCTG
21901 AAATATATTT TGGCACATTC CTTTTTCATG AGTGCATGAA ATCAGATCCG
21951 TACTACTATG GTGGCTAATA TTTTACTCTT AAATCATGTC TTGCCTCTAA
22001 TATATCTGAA AGTATTTTCTG ATGACATACA CATAGCTTTA GCCTAAAAATC
22051 AGCTCCGTCT TGGGTACAAG ACAGAAGACA ACTATAAACA GAAGGTATAC
22101 GATAGGGTAA AATTGCCAGG CAAACAACCT CACTGAGAAA AGGATATCTG
22151 GAGCCCTTCT TTTTATGTGT AAAAAAATCA CTCATAAAT TTTGGCACAG
22201 TGTAAGCATT CACATCATTG TAGAATCAAA GCATAAGAAA TCTGTGATGT
22251 GCTTCTGTAT TGCTTTATTC ATATTCATAT AGTGTTTTCA AGCCATGGTT
22301 TTAAGGGATT GCCAGAATTG GCCATCGTCA CACAGACAGC TGGTAACAGT
22351 TCAACTAGTG CAGCTCATAG CCCAACACTG AGGGCTGCAA TTATTGTCAT
22401 GGGAAGTAAA AGTCATTTAC TGATGAACAT TTCACCTCAG CATGGAAAAT
22451 CCAAATCTCC CCTTAGAAAT TCTTACCCTA TGTGAGAAAT AAAGCACTGA
22501 TATAAATCTG ACCATCAGGA ACAGCAATAG TGTGTAAACA TTAGATGCCA
22551 TTAGAACCAA AATTGACCAT AAGAACCAGA GTTCAGAAAA ATGACTAACT
22601 GCTGTCCTTC ATTATGTATT TCCACTCAAC ATTAGCATTT ATGAAACATT
22651 TTGCACATTA TCCTGTCCTC ACCCTTGCAA TGTTACATTT ATATAATCTG
22701 TGTAAGTGCT CCACTGCCCC ACAGAGTCAT AAGTCCCTGG GACTTGGTGA
22751 TGTGCACAGT GACTGGCACA GAGGGTGAGC TCTGTCGTGC TTGGGAAGAA
22801 AAATGGTCTT CAAATGAATC TTGCCTTGTC TTGAAATGTA TAAACTGCCT
22851 TTTCTAGCAA AAGCATAGAC ACTCTTTCCC TTGGTGACAT GTGCTACGAA
22901 TTCAGCTGGG TTGAGGATCT GGGCTAAATG AACCAAACCT CCCTATACAT
22951 GAAGGATACA CAGAGATGGT GACAGAGAGT GGTCACTTCC GTGAGTGGAT
23001 CTCAATCAAG TCCTCTGAAG CTAATTTCAA TTTTTTTTCT TTAATAAAAT
23051 GATAAAAGTT GTTATTGGCG CTTTTGCTTG TTTATTTCTG ATAACCTAGG
23101 GCTCAGATTT TCAATGTGTC AAATGCTGAC TCACAGCATG GTTCTCCTGA
23151 CAGTTTATTT CATTTAAGGA ACTCTTCACC AGTAAGTTTA TTTACTTGCC
23201 TTGATATCTC CACACATTAA TAATAAAACT AACAAAACCT AATCTGAATT
23251 AAAATCTATC AGCTTTAGGC ATTATTTTGT GTTCTCCTTC TTTCAACATG
23301 GTAAGTGGG TCTCTTTCTT AGGAGCTTGA GAAGATATGA CTGGGGTTTG
23351 TTTTCTCTA CTTCATTTAT TATCTTTCTT TTTTCCAATC AGGTTAGTTT
23401 TTTCTTTTT AGTAAAAGGT GCATAGTAAC TGCTTGAGT ATTGTGTGAA
23451 CAAGTGAATA AATGAAATGA ATTAAGGTAG TGTTTTCACT AGCAGCCCAA
23501 CATTTCTTTC TCTCTAGTA GTGGGTGGGG TATCAGTTAT GGAATGGCAC
23551 CTCCTTCCAG AGGACTGATC ATGTCATTTT CAGCTTATGC TTCCCTTTAT
23601 GCAGTAAAGT TTCCATATTT CCATAAAGAA CAAGAAACCA AATAATCTA
23651 ATGGATATAT AATGAACACA CAGATGAAAA TTTCACCTGC CATGCCTTTG
23701 AAAAAAGATC CCTAGCTACT TGTATTTTCA CTTATAATTA AAATCAGTCT
23751 TTTCACTTAT GTTTTCTTCA GATCTCCTGT TTTGAAGTGT ATATAGATAT
23801 CAACATAGAA ATGCAGCGTA TATTGCTATC AACTGCAGTG GAGCAGTGAT
23851 TCGTAGGTTT TCCAACATCC TTGCCTTAAG CAAACCTGCA AAATCAAAGT
23901 GTGAGCTACG TCTAAACAAT GGGAGAGGCT TTTTTTTTTT TTTTAAGAGT
23951 TAGAACTAAG ACTCTCACTT CCTCCTGTGC CTCCACATTT TTGACCTTCA
24001 CATTGGGCCC CTGCATCAGA ATACAGCACC CCCTAACAGG CTCCTGTTCA
24051 GGAATCTTTC TCTGGAAATA ACAGATGTTG TCTCTAGAGC TGCATAGAAC
24101 CTTAATGGAA TCATTGTGGG TCAGAGGCC TGGATGGTGC TGGGGACCTC
24151 CCTGACCCAC AGCATCTGAC CCACATTTCC AGGTTCTTAG CGACTTGTGT
24201 CAGTAAAGAA AAAGGCACAT AGCTAAGTGG AAGAGCAGAT GAGGCTTGGT
24251 GGAATCAGC CAGTGGTCTG CCCTAGCAAA GGTAACAGA ACTGCTGGGG

FIGURE 3I

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TECH CENTER 1600/2900



24301 GCTTTTGGTC CTAGGCTCAC TACTCAGGGA GGCACCTTAA CATGGAATGA
24351 CCAGCAAGTT TCCTTCCTGA TCTTTTCCAC CACCACCACA AGCCTAGTAC
24401 CTCCCTCCCT CTTTGCTCTG TTGCTCTCTT CGGGAATGCA CTGGAAACCA
24451 CCTTCAGTTC TGTITGGAAT TTTCTTATTC CTTATTGAGA AAGAGGAAGA
24501 AGCTTTTGCA TTTACTCCAA CCGTTCTACC TATTATTCCC ATAAACTTTC
24551 TGTGATCTCA TATCATTAGG CCAAATGTTA ATCTTTCTGG GAGCCAGGAG
24601 ACTGCTTTCA CATTGAGAGG CCCTGGACAT ATAGGACTGC CTCTAACTCA
24651 CTCTAACTCA GCTTATTGAC TTGAATGCAC CTTTTTAACA AGTGACTAAA
24701 AAACAAACTG TGACTATTCT CTGAAAATGA GCCTATATCT CATACTTATT
24751 TATTCTGTTT AACACTGTGA AACAAATTAA GTCCTCTGGC ACTATGTATA
24801 TACCATAAAA AGCTTATTTG TAAGCCTACT AATTGGACCA GTTTTGACAA
24851 TATTGAATAA GCACTAATTG CAGATCATAA TGTAGAATTA TAGGCTGCTG
24901 AGGAAAACAA TATCACACCA TTTGCTTTCC TCAGTTTCCT TTTCAGAATG
24951 AGTTTCATAA TGTTCACTAA TCCAATTTTT AAAATCCTTT ACAAAAGTTAT
25001 TCTTAAACTA TTTCCAGAGA CTATCTGGTT TGTCATTCTA GAAATGAAAT
25051 TGCCTTTTCA GCCTAAACAG ATGGCCTTAA TTTTGGTGG AGTGGTATGA
25101 AAGGAATGTC ACATGAGAAA CTGCAAGCTA TTTAGCTTGA ATTTTTGTC
25151 ATTCATACAT GTTTCAAAAT ATATTTTACA TTTTCTCTCT TTTAAATGAG
25201 TTCCCATCTC TGCACCTTAA GTGACTTCAG AACTAAAATT TTAAAGTGAA
25251 CATCAATCAC AGCATTTCCT AAAATGTGAA CTCCTAGCTT AACCGAAGTA
25301 TTCACCTATT GGAAAGCTGA TAGAGTAATT CCACTAAGTC CAAAAAGTGT
25351 CCTCTAAAAG ATTCCAAAGA TAAGAGTGTT TTCAACTTTG TCAAGCTGTA
25401 CAAACACAAA TGTCCTCCC TCCCTCTGCC CACAGGGATC TTTATCCAGT
25451 TACAGCAGCG TAACTTGAGC AGCTGCTGCA AACTGAGGCT CTCTTGACCC
25501 TTCGCCTACT TATTTGAGCT GCTAAAATAG GGCTGAAATC TGTCAAGGAT
25551 CCTGAAGGGA AGGATAAGAT TCCTACTATT CAATTTAATT TAAGCTTTTA
25601 TTCAGTGCCT GCTGTGTGCA CAACACTAAG CTAGAAAGTC TGAGGAATGT
25651 TTAGATTATT AGGTCTGTG CTTGCTTTT CATAGATTTA CAATCTATTG
25701 ATAGGGAGAG CTAAAAAGGA GAGAAAGAGG AAGGAGCAAA CATAAAAACG
25751 TCAAAATTTT AAAATACCAT TTTAAAATTT TATTTTAAAA TGTTAAATAC
25801 CATGCAAAAT TAAGGAAAAC CTAGATTCAT AAAAAATCCT TTCACAATCT
25851 TGTGTAAATC AATTCAGTGC TTGCCCTTAA TGTCTCATCC AGTCTGATGA
25901 GACATGTTTT GTGATCAACA AGGGTTTTAC TATGTTTCTT AATTATGTGT
25951 CTTGCCTGTT ATCTCTTTCT GACCGAGATT ATTTTAAACA ATAAATTCTG
26001 AAAACTAAGA AAGTGAAAGC ATAAATATT GTCTTATAAA ATACGCCAAG
26051 GAAAAAATGA CACTCCATTT CAAATATCAA AAGTTAGCAT CAAGACTGCA
26101 CAAGATGAAT GTACAGTCAT GTGTTGCTTA CAAATGTGGA CATATTCTGA
26151 GAAATGCATC TTTAGGCAAT TTTGTCATTG TGCAAACACC ATAGATTGTA
26201 CTTGCAGCCT AATTGGTGGA GCCTACTATA CACTAAGGCT ATATGGCATA
26251 GCCTAGTACT CCTAGGCTAC AAACCTGTAC AGCATGTTAC TGACTGAAT
26301 AGTGGAGGTA CCTGTAACAT AATGGTAAGT ATTTGTGTCT CCAAACGTAG
26351 AAAAGCTACT GTAAAAATAC AGTATTACAA CCTTAGGGTA TCACTGTCTT
26401 ATATGTGGTC TGTGTTGAC CGAAATGACT ATGCTTAATA CCACTGAACT
26451 GTACACTTAA AAATGGTTAA GATGGTAAAT TCTATGTTAT GTATGTTTTA
26501 TAATAATAAA AAAATTGAAA AAAGCATCAA CATCTTTTCT GGGAAAAAAG
26551 AAAAAGAAAG AAAATGCATT AGAGTGATGA GAATATTTGA AGTAATAGAT
26601 AAAGTCAAAA ACAAGAAAT GATCTTGCCT TTGAACCTTC TTGTTTAAGA
26651 TTCGTACATC AGTGATCACA CTGTTATTTT CCAAACGACC CTTGAGCTGG
26701 ATACGACATT TCCTGATTGC AGCTGTGCTT ATTGCACTTA ATAATGTTCT
26751 GGTCATCCTT GTGCCAACTA TAAAAACAT CTTCGATTTC ATAGGTGAGT
26801 TTCAGAAAGG CTTCAATTTG GTCAACCCAA ACTCACGCCT CATTAAATGA
26851 TGGACAGGGA ACCAGTGCTG GGTGATCCAG ATCCCCGTTT TTTCTCAGGC
26901 TCATGGATTCT CCTTTATCCC TGCGAGGCTC TGGTGATTGA GCTGCTCACT
26951 GTCTCTTCTT CCTAACTGAC ACTGGGAGCC ACCTTATAGG TCATTTAGTC

FIGURE 3J

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TECH CENTER 1600/2900



27001 AAGCTGCTTT TTCTGATAGA TGAGGAAACT GACCCCTATA AAAGTCAAGT
27051 CATATACCTT GGTGTGGACC CAGGATTTGG ACTTAGGTAT TAGCTCCACC
27101 ATCAGGAAAA GAGGAAGATA GATTTTACCT GCCAGAAGCT CTCTGATACT
27151 ACGAGTATCA GCTGAACATT GAAAGGTATC TTCAGAGGAA TAGGAGGTTG
27201 ATTATATAAA GTGTATTATT AGTATTTCCC CATAACTGCA TGGTCTATTA
27251 ATTTTCATTG TACTCATTGA GGGTTTACTT AAACCTTTAAA CACAATCTAA
27301 AACTTTAAAA GAACCATGGG TAGGTCACCT GCAAAGTAAG AGGTGGATAG
27351 GGTGTGTCAT GAGTTCAGCC ACCTTAGTAT GTATTTATAT TACTAATCCC
27401 CTGTAAATTT GTGTTAAATT CAGCCTTTTG TTGCTTATTA TATGTTGCAT
27451 ATACTTATGC AGCTTTGATG TTAGGTACAT TTTAATTGTC TCTATAAACA
27501 TATCTTCTAT GAATAAATAA CCAAGATGAG CTTATGTGAC TTAAGTGTGT
27551 GTTTTTAGTG CTAAGTATAG GATAGCTTTA TATTTGGTTT ATTTAAAGTG
27601 TGTGCTGGCA TCTCCTTTGC TAGGAACTGC TGGGTAAGAC ATTGACCTTG
27651 CCCTGTGTTT GTCTTCTCAG GGGCTTCTTC TGCCACTATG CTGATTTTTA
27701 TTCTTCCAGC AGTTTTTTAT CTTAAACTTG TCAAGAAAGA AACTTTTAGG
27751 TCACCCCAAA AGGTCGGGGT AAGTAAACCT TGCAATTTCC CCCATTATTA
27801 GTTGTCTTTC CAACTACTTA GAATAAACTA GAAAATACAC ATAGTTCAGA
27851 AAAATGAATC AATGTACAAG AACCAAAAAT CAAAAATGGG CTAGAAGCTT
27901 CTGGTAGCAG AGAAAGGGGA CATATTTCTG AAACCTCAAAT GATTCTACTT
27951 CAAATATCAA ATATCCTGTG TTGAGTCTGT CATACATGTC AAATAGTAGT
28001 AGCCTTTCCC ACAGACACAT ATGCTTCAGG CAAATAGCAG TGTCCAATAC
28051 CAAGCTGCTG TTGTGCTATC CGTGGAAAAT CATGCAAGAA GGAATTAGGC
28101 TCCCTAGCGG TGTTATGGAA TAATTTAAAT ATTTTGGTCA TGGTTGTTAG
28151 GTTTGCAAAG CCAAAGGAAA GATGTTGCTT TTGTTTTCCC TTCCATAGTA
28201 CCTGTTGTCC CTGGTGTGGA CTAAGATCCA GAACAGAACC ATTCATCGTT
28251 CTGTAACTT CTTTAGATAC AAAATACAGT CTTATTAAT TAGAGAGTAC
28301 ATATTTCTTT TCCATAAGAC TACTATAGAA ACAAATGCTA GAAATAATTG
28351 TTTTCCAAT AAGGAAATAT TATCTTTCAC TCCTTAATAA AGTCATGTTA
28401 AGGCTTGAAA AGAATATTTT TTAAGTGAAT ACTCTGAATT TTTACCTTGA
28451 AGTCATTTAC CTTTGGGATG TTCTGGGGAC TTCAGGATAA TTTGGTATCA
28501 AAAGGTCCAC CCAGCAGCTT GCTCCCAAAT TTTAACTCTA TGTAGTCCGT
28551 CTTGCTTGGA TTTTACAGC AGTGTGACCT TGGCAAATTA CTTGTCCTGT
28601 TTGTGACCTA TTTTCAGTTT GACCAATTGT GAAATGAGTA CAATTATCTC
28651 CTAGACCCAT TCTAGTGAAG AATGTTTAGT TGCTGCTTTC TTATATGTAG
28701 GATTAGGAGG TTTAAGTATG TGATAAAATG TAAGGCCTCT TCTGGTGTTA
28751 AAATGCTGAA GTATTTTATA TGTAGGTATG TACATATATC CTTATATATG
28801 TGTGTGTATA TTATATGTAT GCACACACAC ACACACATAT ATACACTTTT
28851 TGTTGCAACA TCTATTAAGC TTTTGGTTTT GTTTGCTTTA TAAAATTAGA
28901 ATCATATCAT ATATGCTATT CTTTTTTAAC CTGCTCTTTT TCACCTAAAA
28951 GATTGTAAGC ATTCTCTAGA TTATTGAATC TTTTCTGTCT CCTTGATTTT
29001 TAATAATCAC AGGGTATTCC ATCATCTTGG TGTACTAAAT CAATTAACCTA
29051 TTAATCCATT GTTGAACCTG TAGGTTGTAT CTCTCCACTG TATTCCTCTT
29101 CTTTCTTCAA CTAGGATTCT AAATTGACTG ATAGGTTAGG CCTGGGCATC
29151 TGAGATATTA AGAATAATAT GGCTCAATAT ATAGATCAGA TTGCCATATT
29201 ATGTAAACAA CTAAAAACA AATTGTAATA AGTATGGTTT CTGTGCTCCT
29251 AACAGAGTCT CTCTGAATTA CAGGCTTTAA TTTTCCTTGT GGTGGAATA
29301 TTCTTCATGA TTGGAAGCAT GGCACCTATT ATAATTGACT GGATTTATGA
29351 TCCTCCAAAT TCCAAGCATC ACTAACACAA GGAAAAATAC TTTCTTTTTT
29401 TATTGGAAAT GGTTACAAGT TATACTCCAA AAGATATTTG AATTATCTTG
29451 ATTGGAATGT TATTCATAGG AAATAACAGG AAGATTCCAA AGACGTTTAC
29501 CAGTAATATC ACCAGGCACC TGCAGAAGAG GAAAATCACT GTTTTTGTCA
29551 AGGATGGTTG TGTATGTGTT TAAAAATAAA CCTGTGGTGC ACATTTCTAC
29601 CCAGGTTTTG CTAGAGCAGT GTGAGATGAT GAAGGTGTAT TTTTGCTGCT
29651 TTACGAGCAG AATAAGGGTA ACTGCATGTA ACAATCATCA GATAGTACTC

FIGURE 3K

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29701 TTTCCCTGC CGTCTCCTCA TCCTGCACCC CCTAAAAAAG TACCAAACAT
29751 TTGCATTCTC AGAACATCAA ACAAAAAATGC CCTGGTGCCA AAGCTATCAC
29801 CATTTAATGT CTTCTCTCAG TCTTGCACCA AAGTCTCTGG TCTGTTTACT
29851 AACAGAGGCA AAAGGCATGT CTTAGGAACT GTTTCTGTTT CTGTAAGGTA
29901 CATGAATGGT CAAACACCAG TCTAGAGCAT CTTATTGTCA ACAGCAAAAT
29951 AATATTTTGC CCACCCTGTT TGTGACATTG AGTTGTGACT TCTATATTCA
30001 ATAGATTTTT GTAAATGTTA AAACATCTAT ATTTAAATGT TAAAAACTA
30051 AATATAGAGA GGGGCTTTAT TTCAATCATA GAGCAACAAC AAAAATAATG
30101 CTTATAGCTA AACTGCCTGT TCTAGAAAGC ATCTGCTTTT TCATGTTATT
30151 CCTAAATCCT CTTGTCATAC TTTTGTCAAT GAACAATGCT CTCCCTCTCG
30201 TCTTCCATCC TCATTAGAA TTTTGTAGAAG ACCACAATCG TGGAGATACA
30251 CTACCCAGTA TTGTTTGATA CATTTTATT TGATAAACAT TCAGTGCAGG
30301 AAAGTGTGAT TTGCTATATG TTTATGTATA TAATCTTATT CTGTAGTCAT
30351 CAGAATGTTA ATGTAAGGTA CATTTGATTT TTATTTTTTA CATGTGTAGT
30401 TTTCTTTCTT CACAGTCAAA GCATTTATAT TATTGGGGGT GGGGGCAGGG
30451 AATTAAGTTG GTGGGCTCGA AAATCCATTC ATATGTATCT GTCTACAAAT
30501 GTCTGGGGAT AATTTAAATT TGAAACCTAA GTTATATATA GTTTGGCAAT
30551 GCTCTTCTTC AATATTTACA ATAATAGGAT GATCTACAAG AAAATAAGTT
30601 TCTTTTGTCA AATTTTATC ATACTAAAGT TGTTCTTTTA ATTTAGCATA
30651 TCTAAAATAG GAATTAGTTC AGTTTAGCTC ACACAGGTGT TTGCTGACAT
30701 TCATTGGCCA TTTAATACAG TGTGAGTGG TTCTCCGTAA AAGTATAAGT
30751 GCTAACACTA CGAAGAAATG CACACGATCA TTCTTGCTCA CTTCTATAAC
30801 AAAGTTACAT AAAATGGATT TAAAAATTCC TACTCACAGC CTAAGACTTC
30851 TGGAGTTCAC TACCTTTTTT TCAAATCATA GTAAGATCAC TTGTGTATTT
30901 TATATTTTAG TAAAGCCAAT TATGAAGTAC AAGTATCATA CACGTACTTT
30951 TGAGCTACTA TTATTTGAAA AAAATCTGCC AAATAGCATC TTTAGGATAT
31001 ATTTACATTT TCACTCATCT AAAAAAGTATA CAAAAATAAA AAGTGGAAAA
31051 AGGTATCTTC TGAATGTTCA AGAGCATCCT ATAGTGCCAA ATAATAAAGC
31101 ACCATTTTTT TCTTCATAAC CAGGATTAAA ATTCATATAT ACTGCAGGGC
31151 AGACATACAT ATGATAGCTT GTGCTGATTA ATTTAACCCC ATTTGTAAAC
31201 AGATGAAAAT TTTATTTTCT TATTTTCAATTA ATAAGATGGC TCAATGTATT
31251 GGGAGGCTTC TTTTTTATTA CAGAAAGTGT ATATTGGTAT ATAATAAATG
31301 AACTTTTCAA ATGACTATGA TGTGATTTTT GATCTATTGT TAAAGAATGT
31351 TGTGTTATTT GTCCATGAAA CAAAAATTTAA AATCCAAATA CTGTCTTTCT
31401 TATATTGGTT TATGTTCCAT TTTCATTGTT ACCTTTGACA CATAACTAAC
31451 ATCTATAGCC ATCATCCTGA AAATAATTGC CATCTTATTT TGGCAAAATA
31501 GATATTTAAT CCTAAATTAT TATGATGATT ATAATTTTGG CATCACATAT
31551 ATACCACCTA GAATGAATGT GGAAGAAATG AGTCTTTTAT GGTTAGTTTG
31601 AAAGAATCCA TTGAAGATAG AAAATGAGAG AATAGAAGAA ACCTGAGAAT
31651 AGTAAAATAA AGAGCAGAGA AAATATGGGG GCAGGGAAAA CATGTGAGTG
31701 CTAAGGATTG ATTATGAATG AACGATTAGG GGGATTGATG GATCACAGGG
31751 TAAGTATATG CTTAACTTTA TAAGAAACTT CCACATAGTT TTCCACAGTG
31801 TTTCTACCAT TTTTATTTCC ACCCGTACTA CCTACAACCT CCACTGACTC
31851 CACAGCCCTG CCAACATTTG GTGTTGTCTT TTGCATTTTA GCCTTTCTAG
31901 TGGGTCTGAA ATGGTAACTC ATTGTGATTT TCATTTCTGC TTCTGTGACA
31951 ACTAATGTTG AAAACTTTTC AAGTGTTTAA TGGTCACTCA TATATCTTCT
32001 TTTGTGAAGT GTGTATTCAA ATCTTTTGCC CATTTTAAAA ATTTAGGTTA
32051 TGTGTTTTTA TTGGGTATTT GTAGAAGCTC TTTAAATATG GATCCATGTC
32101 CAGATTGCCA ATATATTTTC CCAGTCTATG GTATGGTTGC TTATTTTCTT
32151 AAAGGTGTCT TAATTACATC TTTCTGGGGC CAGGTCACCA TAGCTCAAAG
32201 TTTTGCAATT TATGTCTTAA TGAGATAATA TTAATCAGAG TGGTATAGTC
32251 AAAATTAAT GTTTTGATGT CCTGGGCCCA TATAGGTAGG ACTGGATCAT
32301 CTAACCAAGA TGCAAAAAA AAAAAACAAA AAAACAAAAA TAGTACTTGG
32351 AAAAATTAT TTTAAATTAA ACA (SEQ ID NO: 3)

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FIGURE 3L



FEATURES:

Start: 3000
 Exon: 3000-3118
 Intron: 3119-7452
 Exon: 7453-7543
 Intron: 7544-8039
 Exon: 8040-8155
 Intron: 8156-10894
 Exon: 10895-10968
 Intron: 10969-11437
 Exon: 11438-11530
 Intron: 11531-16047
 Exon: 16048-16129
 Intron: 16130-16215
 Exon: 16216-16298
 Intron: 16299-16408
 Exon: 16409-16467
 Intron: 16468-17301
 Exon: 17302-17577
 Intron: 17578-17709
 Exon: 17710-17789
 Intron: 17790-19073
 Exon: 19074-19174
 Intron: 19175-20904
 Exon: 20905-21029
 Intron: 21030-26649
 Exon: 26650-26794
 Intron: 26795-27670
 Exon: 27671-27768
 Intron: 27769-29273
 Exon: 29274-29372
 Stop: 29373

CHROMOSOME MAP POSITION:
 Chromosome 12

ALLELIC VARIANTS (SNPs):

DNA				Protein		
Position	Major	Minor	Domain	Position	Major	Minor
1386	T	C	Beyond ORF(5')			
2594	T	C	Beyond ORF(5')			
2757	G	T	Beyond ORF(5')			
6107	C	T	Intron			
6392	T	C	Intron			
9484	C	G	Intron			
10280	A	G	Intron			
10297	G	A	Intron			
10331	G	A	Intron			
10536	T	C	Intron			
11548	T	C	Intron			
11917	G	T	Intron			
12840	T	-	Intron			
12844	A	-	Intron			

FIGURE 3M

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Docket No.: CL001010

Serial No.: 09/776,705

Inventor: Karl GUEGLER et al.

Title: ISOLATED HUMAN TRANSPORTER PROTEINS...



12847	T	-	Intron
13019	C	-	Intron
13022	A	G	Intron
13285	G	A	Intron
14461	G	C	Intron
15464	-	G	Intron
15469	-	A	Intron
15545	T	C	Intron
16199	T	C	Intron
16798	T	C	Intron
18103	C	T	Intron
18421	A	G	Intron
18528	G	A	Intron
18722	T	C	Intron
18775	C	G	Intron
18951	T	C	Intron
18974	T	G	Intron
19540	A	C	Intron
19841	G	A	Intron
20170	A	C	Intron
20343	T	C	Intron
20519	G	A	Intron
20963	T	C	Exon
21840	G	T	Intron
22783	C	T	Intron
22787	G	A	Intron
22825	T	C	Intron
22967	A	T	Intron
23248	A	G	Intron
23764	G	T	Intron
23765	C	T	Intron
24432	A	G	Intron
24538	C	G	Intron
24693	T	C	Intron
24819	C	T	Intron
25743	C	T	Intron
26044	G	C	Intron
26555	G	A	Intron
27886	A	C	Intron
31884	T	C	Beyond ORF(3')
32229	T	A	Beyond ORF(3')

411

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Context:

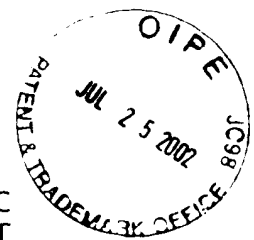
DNA

Position

1386

ACCCATATGCATGTCTTACTTCTATTCTCTCTTAGCTTTTAACTGCTTCTTTTCATCTT
 TTATGTATATACATTTAGGCTGCCTTATATTAATAATAGTTTCATTTTGTTCCTCCTGC
 TTAACCACTGTGTGCTATTTTTTAAATTCTGAGAACTGCTTCTTTATTCTAGACAA
 TTCTCTGCCATTATCTCTTTCTGTTTTGTCTCACCCTAGTCTCACAATTCTCTATATTGG
 AATGACTATCAGTGTATATTTGAACTTGTAATTCTTATTTTTTCCCCATTCTCTTAACT
 [T,C]
 CTTATTTGTATTTTTCTTTTTTAACTCTTTCATGCTATAATTTGAGTGATTTCACAGA
 TCTGTCTTTCAATTTTATAAGTCTTCCCTCAGCTGAGTTTTTTAAATTTCAATGATTCT

FIGURE 3N



ATTTTTTCTTTTTTTTAAGAATTCCTTTTTTGACTCTTTTTGCAACAGCCTGTTCTCC
TTTTATATTCCTTTATAATGTTTTATTCTGTGAAAGTTATTCTTTATTTTGAATGTTT
TCTTTCAAAATGTCTTTCTTTTTATTAATTTAATGTAAAAGTCCCTTTTAAATTGCTTTG
SEQ ID NO: 6

2594 CTGAACCTTTCTTTTGTTACTATTCTTAACTTTGGCTTCAGGATCCAAGTGCTAGAAAAGT
TACTTCCTAAACTTGATCCTCACCTATGTTGCATATTATCAAGCATTTGGTGGTGTAAAT
TCTTTCATGTCCAATTAAATTTAAAGCAGTAATTTCTTTCTAGTTATTGCTAGTAGAGAC
ACTGGTAGATTCTGCCTTGGTAGACCTTCCTCTGTCAACAATTTACTTTTGCTTCCTTT
CTTTTAAACATGTATCCCACTCACAATACCTAAATTTCTTGAAGACTGCTGCCATGT
[T,C]
TTAAGATTTCTTTTTTTTCCATAGTGACTAGTAAAACCTGCCATTTTCATTATACATAG
GCACTCTATAAATATCTGCTAATTTAGCAATTATTAGTAATTTCTTTCTTCTTCCAT
TTCTTCTTTCTTGATTGGGTAAAGGAACATTTCAGGATTTGCTTATGTAAAGTTTTCA
GGAGTTTCTTTCTTCTCCCTTTTACAGAGAGCATACAAAATGTAGATGATTCATATTC
ACTTATTTCAATTAATAAAATTATAATGATGTATGTTGTGTTCTGTTGCAGAACAGAG
SEQ ID NO: 7

2757 TTATTGCTAGTAGAGACACTGGTAGATTCTGCCTTGGTAGACCTTCCTCTGTCAACAATT
TACTTTTGCTTCTTTCTTTTAAACATGTATCCCACTCACAATACCTAAATTTCTTT
GAAGACTGCTGCCATGTTTTAAGATTTCTTTTTTTTCCATAGTGACTAGTAAAACCTGC
CATTTTCATTATACATAGGCACTCTATAAATATCTGCTAATTTAGCAATTATTAGTAATT
TCTTTCTTCTTCCATTTCTTCTTTCTTGATTGGGTAAAGGAACATTTCAGGATTT
[G,T]
CTTATGTAAAGTTTTCAGGAGTTTCTTTCTTCTCCCTTTTACAGAGAGCATACAAAAT
GTAGATGATTCATATTCATTTAATTAATAAATTATAATGATGTATGTTGTGTT
CTGTTTGCAGAACAGAGTGTCTGAACATCAACACAAAGTGAAGAACCTTAAGCTGAAG
GTACAGTATATTATTTACACTGAAGGGGCTTGTTGTGGACAAGAAAGCGCTGACAGCTC
AAATGGATCCCATGGAAGTGAAGAAATGTCAACATCGAACCAGATGATGAGAGCAGCAGTG
SEQ ID NO: 8

6107 GTTTCGTGTGCTGTTTCTATCTACATCTCATACTGTTTTCTATTCTCAAAAAGTAACCCT
GTCATCCTCTTTCTCTCCAGATTATTTTTCAGGATTAGCTTCTGTTATAAAAAATAGCTT
GTACAGATCTCCTACAATAATTATTTTCTATTTTATTTCTAAGGTTTATTTATTTATTTA
TTGAGACAGACAGAGTTTCACTCTTGTTGGCCCATGCTGGAGTGCAATGGTGCAATCTCGG
CTCACTGCAACCTCTGCCTCCAGGTTCAAGCGATTCTCTGCTTCAGCCTCCTGAGTAG
[C,T]
TGGGATTACAGGCGCTGCCACCACACTCGGCTAACTTTTTGTATTTCTAGTAGAGACGA
AGTTTTCAACATGTTGGCCAGGCTGGTCTTGAACCTCTGACCTCAAGTTATCCACCCACCT
CAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGTGCCTGGCCTCTAGGATTAT
ATTAATAGAACAATCTTCAATTATTTTATCTTTCTTTATCTTTCTTTTCATGTAGGAAAT
GTCCTAAAATTTTCAACCCTCAATTTGAAAGCACTTTTAAAATCATACATAGTCGAGCA
SEQ ID NO: 9

6392 CAGCCTCCTGAGTAGCTGGGATTACAGGCGCTGCCACCACACTCGGCTAACTTTTTGT
TTTCTAGTAGAGACGAAGTTTCAACATGTTGGCCAGGCTGGTCTTGAACCTCTGACCTCA
AGTTATCCACCCACCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACTGTGCC
TGGCCTCTAGGATTATTAATAGAACAATCTTCAATTATTTTATCTTTCTTTATCTTTT
TTTTCATGTAGGAAATGTCCTAAAATTTTCAACCCTCAATTTGAAAGCACTTTTAAAAT
[T,C]
ATACATAGTCGAGCATTTTATATAAAAACAACTAAAAAGTCTGTGACATTTTGCAGTATA
AAAATGCAATGGCAGCAGCAGGCTTATTAATTGAGCCTCTTGGAAATGTGGCTGGTCT
AGGTCCGTAGCCTCAAAGGCCCTGGCTTGTAAGTGCAGGAGCTGACCAGCACAGCTCTAT
AACCAAGTTGTACATCTTCTAGCCTGTGTCCAAGAAAACCAGAATCACAACGCTCTGTGG
ATAGTGACATCTTAAAGTTTTCTTTCCCTCCCAACTCTTTTGCCAGTTCATTGAATTGCT
SEQ ID NO: 10

9484 GCAACATTTATATCACAATATGTGCTGTTTATGTTCTGAATATCATATGATTAGTAA
TCACACAGCTATTTGAGGGCTAAGCATCAGGACTATAAATATTTGTATTGTGTTAGTGCT

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FIGURE 30



TTGATTGAACTCTTTTATGTATAATATTCTTCAGCTGAATGGGTTTTATATCAACTTTA
CTTTTATATAAGCCATGTTTTGAAATAAACTAGGATTTTAATAATCTGAATTTTAATAGC
TATGTATGTAGTCATATATTTGTATGCTTTTGTAAATGTGCTTACCTCTAAGACAAAAAAA
[C,G]

CTGCCCTTTCCTTATTAATTATACATACCATTAAAATGAATTAGGAAGTTACAGATCACTG
ATGAATAGAAATAGGAAAAAATCCCCCAATCCCACAGTCATAGATCATCTTCATGAGAG
AAGAATGTTCCACTTTTTAAATGAGGGCCTCATTTTAGGCTTATAAACACTTAGCAGAT
GAATTTGGTCAGAACAAATTAATCACTAAACATCATGGGGTGTGTTTTGTGTGTCTAAGT
AGCCCAGACTGGATTAAGCTTTCTCTCTTAATTTATAGCAAGTGACACAGTATTTTAAAG

SEQ ID NO: 11

10280 ATAAGAGTGCAACATAGCTACAGGGGTTATAAAATTTATAATTCATGGTCCAAATGTACA
TTTGTAGTATTGATTTTCATTGGGAATTACCAAGGGATTAGATCAATTGTGGGGAAAGTGT
ATTTTTTAAAAATAAACAAAGATAAAGATTTTTTTTCTGAATTCAGGTAAAAGGCAGCA
TTGCTCCTCCATTTATTACGTAGATGCTTCTATCAACATTCTTATTTTTGTGCTCCAAAT
CTTGGATTTGAAAAATACCAATCCGTATAAACATAAAGAAACCATACATGCATGTGGGG
[A,G]

TCCTAACACCAGAAATGACTCTGAATGCAAAAAAAAAAAAAAAAAAAAAAGGGAATTTTC
GTGCCCCATCCTTAGCTTTCTGCTTTCTCTATTATATATGCAACTGCCTGCCCTCTA
TCTTACAAAGTACTTCGTAATCTAATGCACAGGATCAGCAGTAATGCAGCTCAGACTGCA
TGCTTTCGCCTTTGGATTCCTAGATTTTCAATTAAGGTTTAGTCAGGCTATTGAATAGCC
CTTCAATTCTAAGTGCTGATGTGAATATCATGCAATATGATGTACATATTCCCATGTGC

SEQ ID NO: 12

10297 CTACAGGGGTTATAAAATTTATAATTCATGGTCCAAATGTACATTTGTAGTATTGATTC
ATTGGGAATTACCAAGGGATTAGATCAATTGTGGGGAAAGTGTATTTTTTAAAAATAAAC
AAAGATAAAGATTTTTTTTCTGAATTCAGGTAAAAGGCAGCATTGCTCCTCCATTTATT
ACGTAGATGCTTCTATCAACATTCTTATTTTTGTGCTCCAAATCTTGGATTTGAAAAAT
ACCAATCCGTATAAACATAAAGAAACCATACATGCATGTGGGGATCCTAACACCAGAAAT
[G,A]

ACTCTGAATGCAAAAAAAAAAAAAAAAAAAAAAGGGAATTTTCGTGCCCCATCCTTAGCT
TTCTCTGCTTTCTCTATTATATATGCAACTGCCTGCCCTCTATCTTACAAAGTACTTCG
TAATCTAATGCACAGGATCAGCAGTAATGCAGCTCAGACTGCATGCTTTCGCCTTTGGAT
TCCTAGATTTTCAATTAAGGTTTAGTCAGGCTATTGAATAGCCCTTCAATTCTAAGTGCT
GATGTGAATATCATGCAATATGATGTACATATTCCCATGTGCTGAGTAAGTAGATGTAG

SEQ ID NO: 13

10331 AAATGTACATTTGTAGTATTGATTTTCATTGGGAATTACCAAGGGATTAGATCAATTGTGG
GGAAAGTGTATTTTTTAAAAATAAACAAAGATAAAGATTTTTTTTCTGAATTCAGGTAA
AAGGCAGCATTGCTCCTCCATTTATTACGTAGATGCTTCTATCAACATTCTTATTTTTGT
GCTCCAAATCTTGGATTTGAAAAATACCAATCCGTATAAACATAAAGAAACCATACATG
CATGTGGGGATCCTAACACCAGAAATGACTCTGAATGCAAAAAAAAAAAAAAAAAAAAAA
[G,A]

GGAATTTTCGTGCCCCATCCTTAGCTTTCTGCTTTCTCTATTATATATGCAACTGCCT
GCCCTCTATCTTACAAAGTACTTCGTAATCTAATGCACAGGATCAGCAGTAATGCAGCT
CAGACTGCATGCTTTCGCCTTTGGATTCCTAGATTTTCAATTAAGGTTTAGTCAGGCTAT
TGAATAGCCCTTCAATTCTAAGTGCTGATGTGAATATCATGCAATATGATGTACATATT
CCCATGTGCTGAGTAAGTAGATGTAGCATTTGCTAATGTTGCTATACATTTAGCATCTAA

SEQ ID NO: 14

10536 TACCAATCCGTATAAACATAAAGAAACCATACATGCATGTGGGGATCCTAACACCAGAAA
TGACTCTGAATGCAAAAAAAAAAAAAAAAAAAAAAGGGAATTTTCGTGCCCCATCCTTAG
CTTTCTCTGCTTTCTCTATTATATATGCAACTGCCTGCCCTCTATCTTACAAAGTACTT
CGTAATCTAATGCACAGGATCAGCAGTAATGCAGCTCAGACTGCATGCTTTCGCCTTTGG
ATTCTAGATTTTCAATTAAGGTTTAGTCAGGCTATTGAATAGCCCTTCAATTCTAAGTG
[T,C]

TGATGTGAATATCATGCAATATGATGTACATATTCCCATGTGCTGAGTAAGTAGATGTA
GCATTTGCTAATGTTGCTATACATTTAGCATCTAAGTTATGAACCAGATTCTACCACTGG

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FIGURE 3P

Title: ISOLATED HUMAN TRANSPORTER PROTEINS...



GTAACATTAAAAAAGTTAGGGACTTCAGGTATGTAAATATAGCAAATCTATTCTA
CGACTTTAAAGGGTATGTGTAGAGTTCTGAAAAGATTTCTCAGCCTCCCCAAATCCAC
ATACTTTTGAAAGCTGATGATTGAAAAGATTAATGTGATCCTTATTGTAACATCTAAC
SEQ ID NO: 15

11548 ACCATTGATTCTTGTTTGGAGAACATTTTGATATATTGCTTATTGGTTTTTGAGGTTGCA
TCTTTTGGGCTTATAATTTCTATATGATGTTTATTACATGTTTGAGACTCCAGCATGGA
ATTATATGACAAAAATATTTTAGTCATTAAACAATCTCTTTAACAAGGCTATTTTATCT
TTGATTGTAGGGTCTTTGATTTATGAAAAATTAGGAGAAAAGGCATTTGGATGGCCGGGA
AAAATTGGAGCTTTTGTTTCCATTACAATGCAGAACATTTGGAGGTAAGGGGATATACTTT
[T,C]
CAATGGATCCCATAAACTTTCTATAGCGTGTTCAATAAATAAGAAAACTTATGGCAATAA
ACAGGCACTTTAGATACAGAAAAATTGCTACTTATAGTTCTTAAATTTTAAATGATAGT
TTCTTAAATAGGTTTGTCCTGCTTTAATTAATAAACAGCAATCTAAGAATGAATAA
CATATAAAACCCTGCCAATTGAATTCAGAAATTAATAATAAAATGAAGCTTTCTTGAT
TTTTAATGTTATTATAGCATGAATTACTCTTAAAAATTGAAGAATTTGTGCTTATAT

11917 TTTAGATACAGAAAAATTGCTACTTATAGTTCCTTAAATTTTAAAAATGATAGTTTCTTAAA
TAGGTTTGTGTCCTGCTTTAATTAACCAAGCAATATCTAAGAATGAAATAACATATAAAA
ACCCTGCCAATTGAATTCTAGAATTAATAATAAAAAAGCTTCTCTGATTTTTAATG
TTATTATAGCATGAATTATTACTCTTAAAAATTGAAGAAATTGTGCTTATATCTGTCATT
GACAAAACAGTTGACGTTTTCTATGTGTGACTGAGTTCGATTTACTAACTGAAAAGTGG
[G, T]
TGTCTGGGGGAACATAGCCAAATGCTGTGGTCCTTGAAACGCAGCCTGCACTGAGCCAGC
CCACTAGACAGTGTCTCTGGAAGTTTACTAAGGCAAAAGTCTGGCTAGGCATCAAATGCA
CTATAAAACCCCGGTTTGTTGATTCATGGAATCTTATAATCCCCTGAAATTATCATTTT
CAGTGTAGGACCTAGAAATATATATATATTTTTTAACAATGTTCTCTCGTTGGTGTGTT
TGCCACACAGCTTCATACTGTTTCTGTTGTGTCCTTTGGCCCTCAGAAGGCATCCAAACCC

12840 GACTATTGCAGTAGTCTTCTAACTGGTCTTCCTGGCTTGAGTTTCCCCTGCTCTCAGATA
AACTCTAATTTGTTCTCCAGATAAACTTTCTCAAATTTGAGTCTGTTTCTACTTTTGTCTG
TGCATAAAATTCCTCAGCATGCCTTTATTATTTTCAAGGAAAAACTTAAACTCATTGGAC
TGACACAAGATCTTCGTCTAGTTCCTCTGCTCAATCTTTCTAAACTTTCCTAGCAATGCG
CATATCTATCTATCTTTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT
[T, -]
ATCATCTATCAATTTATCCATCATCTATACCCTACATGTCCTGTGTCAAACCATAACAAA
TTATATTTATTTCCCCTAACAGTACTATTTTAATATTTTAAAAATCATCCATGCCTTCTT
TTCACAGGCTACTTTCTCCCCTTGACTGCTCTCAAAGTCCTCCAACCCCTAACACACACG
CACACACACACACACACACACACACACACACATTTTCTCTCTCACTCTGCTCAC
CTGGTCTATTGCTCCTCTAGACTGGTAAATACTAGTTCCTCTGGGCTCTCATGGTCTGT

12844

SEQ ID NO: 18

ATTGCAGTAGTCTTCTAACTGGTCTTCCTGGCTTGAGTTTCCCCTGCTCTCAGATAAACT
CTAATTTGTTCTCCAGATAAACTTTCTCAAATTTGAGTCTGTTTCTACTTTTGTCTGTGCA
TAAATTCCTCAGCATGCCTTTATTATTTTCAAGGAAAAAAGCTTAACTCATTGGACTGAC
ACAAGATCTTCGTCTAGTTCCTCTGCTCAATCTTTCTAAACTTTCCCTAGCAATGCCATA
TCTATCTATCTTTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATC
[A, -]
TCTATCAATTTATCCATCATCTATACCCTACATGTCCTGTGTCAAACCATAACAAATTAT
ATTTATTTCCCCTAACAGTACTATTTTAATATTTTAAAAATCATCCATGCCTTCTTTTCA
CAGGCTACTTTCTCCCCTTGACTGTCTCTCAAAGTCCTCCAACCCCTAACACACGCACA
CACACACACACACACACACACACACATTTTCTCTCTCACTCTGCTCACCTGG
TCTATTGCTCCTCTAGACTGGTAAATACTAGTTCCTCTGGGCTCTCATGGTCTGTTTG

SEQ ID NO: 19

12847 GCAGTAGTCTTCTAACTGGTCTTCCTGGCTTGAGTTTCCCTGCTCTCAGATAAACTCTA
ATTTGTTCTCCAGATAAACTTTCTCAAATTTGAGTCTGTTTCTACTTTTGCCTGCATAA

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FIGURE 3Q



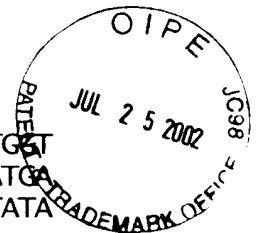
- CATTCTGAATTTTTGAAGACCAACATGTTAACATCACTGACATCACTGAAAACCAGCAA
TTAATAGCTGTAACATTGAATGGTACCTACCAAGCCAGCTAATCAGAAATATCTCCTGT
GTTCACTCTGTAAGATTTAGCTTTAGCCAAGGTCTTTGCAAAGATTAACCAAATAATG
SEQ ID NO: 24
- 15464 TGAGTTCTATTTTTAACTGAATCTTTTGCCCATGTGTCAACAAATTAACGTTATCCTTCA
CCAAATGGGTGGGCTTGAAAAAGGCGTGATGCATAAATATTTACAGTTGTAGGCAAAATT
GTAATGTTATGTATATGAATACATATTCATTTTTTCAGGGAGAAGGCTTGAGATTTTCAT
CAAGAAATCTTTCACAAGAGTAGATAATCATTATGTATCACTTACCTAGATGCTCATGA
AATTTTGCCACTTTATATAATTCCTTAGTTAGCCAAAAGGAGAGTAAGATGAAGAGGGGG
[-,G]
AAAAAAAAAACTTCTTTGACAAAGATGGAGAGAAGCTGTCATCTCTTGATTCTTTTATC
AATCCAGGAAGCCTTTGGTTTTGACAATAAGTGGTCTGAGACTTTGTGTA CTCTCAGAT
AGGTCCCGGAGGACTAGATTGGTGCCCATCTGCAGAAAACCAGAGGGGATATATTGACTC
TGCAGATCTGCCCTTTGATTCTGCCATCTCTCAGCTGGCCCATGCCTTTTGTGTCAGAC
TACTGCCCAAGTTATAGACACTAACACAGGCACACTGAGTATGGGCTATGTTGATTTATA
SEQ ID NO: 25
- 15469 TCTATTTTTAACTGAATCTTTTGCCCATGTGTCAACAAATTAACGTTATCCTTACCAAA
TGGGTGGGCTTGAAAAAGGCGTGATGCATAAATATTTACAGTTGTAGGCAAAATTGTAAT
GTTATGTATATGAATACATATTCATTTTTTCAGGGAGAAGGCTTGAGATTTTCATCAAGA
AATCTTTCACAAGAGTAGATAATCATTATGTATCACTTACCTAGATGCTCATGAAATTT
TGCCACTTTATATAATTCCTTAGTTAGCCAAAAGGAGAGTAAGATGAAGAGGGGGGAAAA
[-,A]
AAAAACTTCTTTGACAAAGATGGAGAGAAGCTGTCATCTCTTGATTCTTTTATCAATCC
AGGAAGCCTTTGGTTTTGACAATAAGTGGTCTGAGACTTTGTGTA CTCTCAGATAGGTC
CCGGAGGACTAGATTGGTGCCCATCTGCAGAAAACCAGAGGGGATATATTGACTCTGCAG
ATCTGCCCTTTGATTCTGCCATCTCTCAGCTGGCCCATGCCTTTTGTGTCAGACTACTG
CCCAAGTTATAGACACTAACACAGGCACACTGAGTATGGGCTATGTTGATTTATAACTAA
SEQ ID NO: 26
- 15545 AGGCGTGATGCATAAATATTTACAGTTGTAGGCAAAATTGTAATGTTATGTATATGAATA
CATATTCATTTTTTCAGGGAGAAGGCTTGAGATTTTCATCAAGAAATCTTTCACAAGAGT
AGATAATCATTATGTATCACTTACCTAGATGCTCATGAAATTTTGCCACTTTATATAAT
TCCTTAGTTAGCCAAAAGGAGAGTAAGATGAAGAGGGGGGAAAAAAAAAACTTCTTTGAC
AAAGATGGAGAGAAGCTGTCATCTCTTGATTCTTTTATCAATCCAGGAAGCCTTTGGTT
[T,C]
TGACAATAAGTGGTCTGAGACTTTGTGTA CTCTCAGATAGGTCCTCGGAGGACTAGATTG
GTGCCCATCTGCAGAAAACCAGAGGGGATATATTGACTCTGCAGATCTGCCCTTTGATTC
TGCCATCTCTCAGCTGGCCCATGCCTTTTGTGTCAGACTACTGCCCAAGTTATAGACAC
TAACACAGGCACACTGAGTATGGGCTATGTTGATTTATAACTAATGAGGGCAGAACCTTA
GAAGTGCAGCTTCACTGTAACTTTGGAGCAGGATTTAACACAGAATCAGCCCTGATACT
SEQ ID NO: 27
- 16199 AGAACTTGGAAGCAGTGCCAAATACACAATGACTTTTTTTCCATTTGGGGGATTAGATG
TTCATCTTACATATCCCAAATGTCATAACTTGCTTGATGTGACTTCAGTACTGTCCACA
CCATTAAGCTGTCACATTTCCATTTTAGCAATGTCAAGCTACCTCTTTATCATTAATA
TGAAGTACCTGAAGTAATCAGAGCATTATGGGACTTGAAGAAAATACTGGGTATGTCTT
ATGCTCCCTCTGTGACATCAAGTACTTCTACTTGGTCTTTCTGATTCTAATATCC
[T,C]
TGTCTCTCACTTCTAGAGAATGGTACCTCAATGGCAACTACCTCATCATATTTGTGTCTG
TTGGAATTATTCTTCCACTTTGCTCCTTAAAAATTTAGGTAAAGATATTTCTAACTGG
AAATATTTTTATTTTTATTTACATTTAAATAGGTTAGCTAATTGTAGATGCCATATTCA
CCTTCCAAAATGCTTCTTCTAACTTCTAGGTTATCTTGGCTATACCAGTGGATTTTCTCT
TACCTGCATGGTGTTTTTTGTAGTGTGGTAAGTGATGTGATGACATGATCCTTGACAGGT
SEQ ID NO: 28
- 16798 GTTGGTTAGCATGAGTTTTTTTTGTGCCTAAATTAGTGTCTCATTTTGTTCAGCACTTC
ACTAATATGAAATAGTTCTTGATCACAAGTGATTTTCTTGAGACTAATTTAGAGCAAA

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FIGURE 3S



AAAAGAGCAGCTACGATTTAAAGATAGTTGAGGTAGAATATCAAAGCTACTACTAATGCT
TTGGTCTAGGCACACTGGTTATATATGCGGAAAAAAGGAAAACTTCAAGCAGGAACATGA
CAATAATCTGGCATTTAGAACAGCAGAGGAGAGTCCCAGATGAGAAACAAGAAGGCTATA
[T,C]

CCATATTCACATGAATCAGCCATTCTCTCTTACACATTCCACCCATTAAGAGAGGACAAG
AACAGTGGGATTAAAGAAGAAATCCTCCTCTAGGCCCTGACAAAAGAGGGAATTTCT
TGCATATCATGAATGCCAAAATTTATAAAGCATTTCCTCAAGAGGTAAAGGAGAAGGA
AAAAAAGTTTTGAAGACCCATGTCACCTTAGTTTGAAGAAATAAGGAAATGATCATCTTT
CTCATGGAAGGGCATGAAAGAGGGTGGGAAGGATTCTTGCAAAATATTGTCCTGTTAACT

SEQ ID NO: 29

18103 CATTTTAGCATTCTAATTTGCTTTGAAATTCTGCTCATATGTTCAAAGATTCTTTAACAG
GAAACACAGTTTATAGCTTCTCTTTCAGAGAAAATATGTACTCCATCCACTCCTCAGTAA
CATGCTTTAATCAGAAAGTGGAATCAGCCCACCACAGCACTACCTTATCTTCTTCTC
TCCTTCTCTCCACCATAATGGTTCAGGGGAGGGGTTTCATGGCAGGTGGACAAGGAGTCG
ATGGTTGTAATAATTTTGGCAGGTGTTGGGAATTTAAATTTGAATTTTGTTCGGAAGAAA
[C,T]

GATGTCAGCTGGACTAGAAATGAAAACACCCATGACGACCAAACTTATGGTTAGGGGCA
GCCTCGATAAGCCAGTGATGTCATTTATAGTCAGCACCTAACCTTGTCTAGAACACATT
CATTACAAGAGATGTGTCAATATCTGCTTTGTTGTCTTATTTGTACAATAGAGTCACT
GGCTAGAAAATCTTGTTCTTCCAGCTGATGGTCTATGGTTCAATTTGATTCTTTTCCCT
TTGAAGTTGTTGATATTTGCTTGGGAACAAAGGATATGAACTCATTATAGCTGTTTCT

SEQ ID NO: 30

18421 AAATGAAAACACCCATGACGACCAAACTTATGGTTAGGGGAGCCTCGATAAGCCAGTG
ATGTCATTTATAGTCAGCACCTAACCTTGTCTAGAACACATTATTACAAGAGATGTGT
CAATATCTGCTTTGTTGTCTTATTTGTACAATAGAGTCACTGGCTAGAAAATCTTGTT
TCTTCCAGCTGATGGTCTATGGTTCATTTGATTCTTTTCCCTTTGAAGTTGTTGATATT
TGCTTGGGAACAAAGGATATGAACTCATTATAGCTGTTTCTCTTTTCCCTTAAAGGAGG
[A,G]

TATTATATAATAATTCTCAACTTCTTTAATCTAGACATCAGTAACCTCAGTCTTCATTCT
CACTAAATAGCAAACTTTCCCATAAATTTCTGATTTACCTCATAAAAAATTTCAGAACA
CTTTCAAGTATTTTGATGCTTTGATTTACTTTGAAAATTACATGTAGCAGTTACTCCAG
AAGCCTGACAATTGATCTTTGGCAGCCAGGTTCTTCTAGAATGGTTTTGAGAAGCTTTT
CAGGTAGTCTGGACTCCTGGCAGTAGTACTTTGCTGACTCTACTAGGTTCTTTTCCCTCAT

SEQ ID NO: 31

18528 ACAAGAGATGTGTCAATATCTGCTTTGTTGTCTTATTTGTACAATAGAGTCACTGGCT
AGAAAATCTTGTTTCTTCCAGCTGATGGTCTATGGTTCATTTGTATTCTTTTCCCTTTGA
AGTTGTTGATATTTGCTTGGGAACAAAGGATATGAACTCATTATAGCTGTTTCTCTTT
CCTTTAAGGGAGGATATTATATAATAATTCTCAACTTCTTTAATCTAGACATCAGTAACC
TCAGTCTTCATTCTCACTAAATAGCAAACTTTCCCATAAATTTCTGATTTACCTCATAA
[G,A]

AAATTTGAGAACACTTTCAAGTATTTTGATGCTTTGATTTACTTTGAAAATTACATGTA
GCAGTTACTCCAGAAGCCTGACAATTGATCTTTGGCAGCCAGGTTCTTCTAGAATGGTT
TTCAGAAGCTTTTCAGGTAGTCTGGACTCCTGGCAGTAGTACTTTGCTGACTCTACTAGG
TTCTTTTCTCATTTAAAGTCATCTCATTATGAAATGCAAAAGCTTTCTATGTTAGGAGC
CTGTTTCATCTTTATGTTAATTATATTCTTATTAGTGGGCAAGCTTACTGACCTACGTG

SEQ ID NO: 32

18722 TATTATATAATAATTCTCAACTTCTTTAATCTAGACATCAGTAACCTCAGTCTTCATTCT
CACTAAATAGCAAACTTTCCCATAAATTTCTGATTTACCTCATAAAAAATTTCAGAACA
CTTTCAAGTATTTTGATGCTTTGATTTACTTTGAAAATTACATGTAGCAGTTACTCCAG
AAGCCTGACAATTGATCTTTGGCAGCCAGGTTCTTCTAGAATGGTTTTGAGAAGCTTTT
CAGGTAGTCTGGACTCCTGGCAGTAGTACTTTGCTGACTCTACTAGGTTCTTTTCCCTCAT
[T,C]

TAAAGTCATCTCATTATGAAATGCAAAAGCTTTCTATGTTAGGAGCCTGTTTCATCTTTA
TGTTAATTATATTCTTATTAGTGGGCAAGCTTACTGACCTACGTGAAATAGACTGTTCC

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FIGURE 3T



- TCTTCTAGGGAAATGATTGTTTTTAAGACTGAAGGACTAGTGTTTAAGAAAAATGGAAAT
GAATCCTCATTAGCTCTCTAAGACAAATTTAAATCAGCTATAAGTTTATGTACTAAATA
GTCTTCATGATTAGCAATATAGATATACTTTTTTATTATTATTTTCATTTTGAAAAGTGA
SEQ ID NO: 33
- 18775 TCATTCTCACTAAATAGCAAACTTTCCCATAAATTCTGATTTACCTCATAAAAAATTT
CAGAACACTTTCAAGTATTTTGATGTCTTTGATTTACTTTGAAAATTACATGTAGCAGTT
ACTCCAGAAGCCTGACAATTGATCTTTGGCAGCCAGGTTCTTCTAGAATGGTTTTCAGA
AGCTTTTCAGGTAGTCTGGACTCCTGGCAGTAGTACTTTGCTGACTCTACTAGGTTCTTT
TCCTCATTTAAAGTCATCTCATTATGAAATGCAAAGCTTTCTATGTTAGGAGCCTGTTT
[C,G]
ATCTTTATGTTAATTATATTCTTATTTCAGTGGGCAAGCTTACTGACCTACGTGAAATAGA
CTGTTCTCTTCTAGGGAAATGATTGTTTTTAAGACTGAAGGACTAGTGTTTAAGAAAA
TGGAAATGAATCCTCATTAGCTCTCTAAGACAAATTTAAATCAGCTATAAGTTTATGTAC
TAAATATGTCTTCATGATTAGCAATATAGATATACTTTTTTATTATTATTTTCATTTTGA
AAAGTGATTTTTTTTTGTAAGTTTAAAAACAAAGCTTGGTGTTCTTTCTTTTCCAGTC
SEQ ID NO: 34
- 18951 CAGAAGCTTTTCAGGTAGTCTGGACTCCTGGCAGTAGTACTTTGCTGACTCTACTAGGTT
CTTTTCTCATTTAAAGTCATCTCATTATGAAATGCAAAGCTTTCTATGTTAGGAGCCT
GTTTCATCTTTATGTTAATTATATTCTTATTTCAGTGGGCAAGCTTACTGACCTACGTGAA
ATAGACTGTTCTCTTCTAGGGAAATGATTGTTTTTAAGACTGAAGGACTAGTGTTTAAG
AAAAATGGAAATGAATCCTCATTAGCTCTCTAAGACAAATTTAAATCAGCTATAAGTTTA
[T,C]
GTACTAAATATGTCTTCATGATTAGCAATATAGATATACTTTTTTATTATTATTTTCATT
TTGAAAAGTGATTTTTTTTTGTAAGTTTAAAAACAAAGCTTGGTGTTCTTTCTTTTCC
AGTCGGTCCCGAGAAAAATGCAAACGGTGCAAAATTTTCCATCACGGGGATGCTTGTC
ATGTACCTGCTTGCCGCCCTCTTGGTTACCTAACCTTCTATGGTAGGTCACCTGAAAG
TCATTCTCTATATGCAAATCCTTGTTAGGCTGGTCCTTGACCTGGGTAGGTATGATTTTT
SEQ ID NO: 35
- 18974 ACTCCTGGCAGTAGTACTTTGCTGACTCTACTAGGTTCTTTTCTCATTTAAAGTCATCT
CATTATGAAATGCAAAGCTTTCTATGTTAGGAGCCTGTTTCATCTTTATGTTAATTATA
TTCTTATTTCAGTGGGCAAGCTTACTGACCTACGTGAAATAGACTGTTCTCTTCTAGGGA
AATGATTGTTTTTAAGACTGAAGGACTAGTGTTTAAGAAAAATGGAAATGAATCCTCATT
AGCTCTCTAAGACAAATTTAAATCAGCTATAAGTTTATGTACTAAATATGTCTTCATGAT
[T,G]
AGCAATATAGATATACTTTTTTATTATTATTTTCATTTTGAAAAGTGATTTTTTTTTGTA
AGTTTAAAAACAAAGCTTGGTGTTCTTTCTTTTCCAGTCGGTCCCGAGAAAAATGCA
AACGGTGCAAAATTTTCCATCACGGGGATGCTTGTCATGTACCTGCTTGCCGCCCTCTT
TGGTTACCTAACCTTCTATGGTAGGTCACCTGAAAGTCATTCTCTATATGCAAATCCTT
GTTAGGCTGGTCCTTGACCTGGGTAGGTATGATTTTTTAAAAATTGCCTTCTATAAGCATG
SEQ ID NO: 36
- 19540 GGTATGATTTTTTAAAAATTGCCTTCTATAAGCATGCTCTATAGATGACACATATTCAATT
AATACTATTTTAGTTTTGTCACTTGACCTGAGGAAATGGGGCCTGATTCAGCCTGGCT
AACAAGTTACAAGAATTTGTGAATTAACACCTATTTTATAAAAAATATCCCTCAACAAA
ATTATTTTCTCTAGGGATAGATGATTTTCTCTGGCTAGACTCCATAGTCCAACCTCAGG
CTACAAGTGATGAGAATGAATCCACTTGCATGTGATAAAGCTCCTTTGATGGAATTATTA
[A,C]
CTGCCACACAAATAGCAGGGAACTGCCAGGTCCTCAAGTTTGAATTTGCCTCCTCTTTA
CCAGTCAAGTCAAATCTGGGAGCTTGGGACTTTAGGTAAAATTTCTGACATATCCCATTCT
TATTTTGTATACTAAATGATTTCTAAGAAAGAGGACATGACAGAATTTCTTCAATCT
AAGAATGCACCACCAAAAAAAGTGACTATGGCCACATTAGATTATGCCTGCAACATTTCT
CTCTCTGGCATCTTAACAGTTCAAAAGGAGTAGGATTGTACTCCTTCCATGAAGTGTG
SEQ ID NO: 37
- 19841 CTGCCACACAAATAGCAGGGAACTGCCAGGTCCTCAAGTTTGAATTTGCCTCCTCTTTA
CCAGTCAAGTCAAATCTGGGAGCTTGGGACTTTAGGTAAAATTTCTGACATATCCCATTCT

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FIGURE 3U



TATTTTGTATACTAAATGATTTTCCTAAGAAAGAGGACATGACAGAATTTCCCTTCAATC
AAGAATGCACCACCAAAAAAAGTGACTATGGCCACATTAGATTATGCCTGCAACATTTCT
CTCTCTGGCATCTTAACAGTTCACAAAGGGAGTAGGATTGTACTCCTTCCATGAAGTGTG
[G,A]

CCACATAACAGATTTTCATGGAATCACATATTGACCTGGTAGCATATGTTTACATGAATC
AGTGTATCAATATAAATATATTTTTGTATAAACCTCCTTTTAAAGTTTTTAACCTTAATTT
TTTTCTTACTGACTTGGTAAATTGAATTGCATGTATGACAAATTGTGGAGGAAAAGATTC
AGGAGTAGGCCACCATTGTCTTAGGTTTTTTTTCTATTTGACTAATATTTGACTATTAAC
CAACATGTGCTTTAGATTGGGCATTAACTTTTTGCCGGTTGTGAAATAATGAATGACGA

SEQ ID NO: 38

20170 TATTGACCTGGTAGCATATGTTTACATGAATCAGTGTATCAATATAAATATATTTTTGT
TAAACCTCCTTTTAAAGTTTTTAACCTAATTTTTTTCTTACTGACTTGGTAAATTGAATT
GCATGTATGACAAATTGTGGAGGAAAAGATTGAGGAGTAGGCCACCATTGTCTTAGGTTT
TTTTCTATTTGACTAATATTTGACTATTAACCAACATGTGCTTTAGATTGGGCATTA
CTTTTTGCCGGTTGTGAAATAATGAATGACGAGGTCAATACTACTGAAGGTATTTTCACT
[A,C]

CTTTTTGTCTGATCTTGAGGTGAAATCCAACCTACGCTTGATTCCATAGATATTTTCTTG
TTATTTGTGCTTGGAGTCTGAATGAAGGTGTTTTCAAGTAGGGCTGCATCTTCGTCTTA
GAGTAGTACCCACTGGGAGACCCTCTAAAAATTATACTAATTTATCCCTGCACGTTACTT
ATACTTATTTTAATGAGTTTCATAAGACAAGCAAAAACTTGAAAGAGCCCCAAAAATATCT
GTTTTAGTGTGGTGATGGAGTCATAGTTGTTGAGCTTGAAAAATGGTAGCAATCATTCA

SEQ ID NO: 39

20343 TAGGTTTTTTTTCTATTTGACTAATATTTGACTATTAACCAACATGTGCTTTAGATTGG
GCATTAACCTTTTTGCCGGTTGTGAAATAATGAATGACGAGGTCAATACTACTGAAGGTAT
TTTCACTACTTTTTGTCTGATCTTGAGGTGAAATCCAACCTACGCTTGATTCCATAGATA
TTTTCTTGTTATTTGTGCTTGGAGTCTGAATGAAGGTGTTTTCAAGTAGGGCTGCATCT
TCGTCTTAGAGTAGTACCCACTGGGAGACCCTCTAAAAATTATACTAATTTATCCCTGCA
[T,C]

GTTACTTATACTTATTTTAATGAGTTTCATAAGACAAGCAAAAACTTGAAAGAGCCCCAA
AATATCTGTTTTAGTGTGGTGATGGAGTCATAGTTGTTGAGCTTGAAAAATGGTAGCAA
TCATTATCTAGAGTTTACACACTGGGTTTGTAACTGCATCAGGAGTGGCTGCACAGG
TAGGGACAGGGGAGGTGGTAGGCTGGGAGAGACAATATGTGGGGCTTGGGTCTCTCATCC
CCTTCAACAAGAGCACCTTGGTCTCTGTCTGATTTGTAATTGCTTCTGTACAGCGGAGAT

SEQ ID NO: 40

20519 GATATTTTCTTGTTATTTGTGCTTGGAGTCTGAATGAAGGTGTTTTCAAGTAGGGCTGC
ATCTTCGTCTTAGAGTAGTACCCACTGGGAGACCCTCTAAAAATTATACTAATTTATCCC
TGCACGTTACTTATACTTATTTTAATGAGTTTCATAAGACAAGCAAAAACTTGAAAGAGC
CCAAAAATATCTGTTTTAGTGTGGTGATGGAGTCATAGTTGTTGAGCTTGAAAAATGGT
AGCAATCATTATCCTAGAGTTTACACACTGGGTTTGTAACTGCATCAGGAGTGGCTGC
[G,A]

CAGGTAGGGACAGGGGAGGTGGTAGGCTGGGAGAGACAATATGTGGGGCTTGGGTCTCTC
ATCCCCTTCAACAAGAGCACCTTGGTCTCTGTCTGATTTGTAATTGCTTCTGTACAGCGG
AGATAGATTTATCACAATGTAATGAGCTTGAGAGGCTCTTTATTTTGATTATACCTTC
TGCAACGTTATCAGCTTCAGGACCTCTTTGTTCAATTTGAATGAAGGTTGCATAGCTAATG
AGCTCAGAGGCAAGACCAGAGGTGCCTGGATTCCAGGCCTAGGCTTTTCTCTGTTCT

SEQ ID NO: 41

20963 TGAGCTTGAGAGGCTCTTTATTTTGATTATACCTTCTGCAACGTTATCAGCTTCAGGAC
CTCTTTGTTCAATTTGAATGAAGGTTGCATAGCTAATGAGCTCAGAGGCAAGACCAGAGGT
GCCTGGATTCCCAGGCCTAGGCTTTTTCTCTGTTCTGTGTTCTCTCTATAAAATGTTGC
CATAAGTGACCTGTGCTGATTTGACAACACCAAGCGGTTTCATTCTCTTTTCTGTTGT
AGGAGAAGTTGAAGATGAATTACTTCATGCCTACAGCAAAGTGTATACATTAGACATCCC
[T,C]

CTTCTCATGGTTGCGCTGGCAGTCTTGTGGCAGTAACCTAAGTGTGCCCATTTGTCCTC
TTCCCAGTAAGTACATAAGACTTTGATGAAAGAAACCTACTTGACCCCATAAATTAGTAC

FIGURE 3V



ATGTGTTCTACCTTCATTTTGAATTAATTATAGGGTGAGTTTGCAATTGCAATGCCTGAG
GATATTATTTTCTATAGCATTTTGAGTCACTTAAAATTGGCCATTTAATGTGTAGATAG
AGCAAGTAGTTTCAGGTGGTATTTTATAGTGTAGGAAAAAATCATAAAACCTATTTTT

SEQ ID NO: 42

21840 AAACAGTTATGCTATCTATCACATATCTCTCACACATGGCCTCTGCCAGACTCACACC
AGGTCACCCCTCCCTGGCATTTGTCTTGGTGTGAGTTTGTCTGAGATCCCAGAGCAGA
GCTGGTAGTGAAGATTTGGGCTGTGTGAGTTAAAACCACCACCTAAGGATAAACACAGGT
CTTCAACCCTCCTGCCAGCTCCTGTTTCATAAACACTGAATTTACTCATTCAATTTGAGGGG
GAAAAAATAAGTGACACAGTAACCAGCACTGTCCTGGACATAATGTTCCATACAGGGCT
[G,T]

GCATATGAAGACTATTTCTATAATGACACTGTGGTCACTTTAAATGCAGCTTGTGTGCTG
AAATATATTTTGGCACATTCCTTTTTCATGAGTGCATGAAATCAGATCCGTAATACTATG
GTGGCTAATATTTTACTCTTAAATCATGTCTTGCCTCTAATATATCTGAAAGTATTTTCA
ATGACATACACATAGCTTTAGCCTAAAATCAGTCCGTCTTGGGTACAAGACAGAAGACA
ACTATAAACAGAAGGTATACGATAGGGTAAAATTGCCAGGCAACAACCTTCACTGAGAAA

SEQ ID NO: 43

22783 TGAGAAATAAAGCACTGATATAAATCTGACCATCAGGAACAGCAATAGTGTGTAACATT
AGATGCCATTAGAACCAAAATTGACCATAAGAACCAGAGTTTCAAAAAATGACTAAGTGC
TGTCTTTCATTATGTATTTTCACTCAACATTAGCATTTATGAAACATTTTGCACATTATC
CTGTCTCACCCTTGCAATGTTACATTTATATAATCTGTGTAAGTGCTCCACTGCCCCAC
AGAGTCATAAGTCCCTGGGACTTGGTGATGTGCACAGTGACTGGCACAGAGGGTGAGCTC
[C,T]

GTCTGTCTTGGGAAGAAAAATGGTCTTCAAATGAATCTTGCCTTGTCTTGAATGTATAA
ACTGCCTTTTCTAGCAAAAGCATAGACACTCTTCCCTTGGTGACATGTGCTACGAATTC
AGCTGGGTTGAGGATCTGGGCTAAATGAACCAACCTCCCTATACATGAAGGATACACAG
AGATGGTGACAGAGAGTGGTCACTTCCGTGAGTGGATCTCAATCAAGTCTCTGAAGCTA
AATTCAATTTTTTTTCTTTACTAAAATGATAAAAGTTGTTATTGGCGCTTTTGCTTGTTT

SEQ ID NO: 44

22787 AAATAAAGCACTGATATAAATCTGACCATCAGGAACAGCAATAGTGTGTAACATTAGAT
GCCATTAGAACCAAAATTGACCATAAGAACCAGAGTTTCAAAAAATGACTAAGTGTCTGTC
CTTCATTATGTATTTTCACTCAACATTAGCATTTATGAAACATTTTGCACATTATCCTGT
CCTCACCCTTGCAATGTTACATTTATATAATCTGTGTAAGTGCTCCACTGCCCCACAGAG
TCATAAGTCCCTGGGACTTGGTGATGTGCACAGTGACTGGCACAGAGGGTGAGCTCTGTC
[G,A]

TGCTTGGGAAGAAAAATGGTCTTCAAATGAATCTTGCCTTGTCTTGAATGTATAAACTG
CCTTTTCTAGCAAAAGCATAGACACTCTTCCCTTGGTGACATGTGCTACGAATTCAGCT
GGGTTGAGGATCTGGGCTAAATGAACCAACCTCCCTATACATGAAGGATACACAGAGAT
GGTGACAGAGAGTGGTCACTTCCGTGAGTGGATCTCAATCAAGTCTCTGAAGCTAAATT
CAATTTTTTTTCTTTACTAAAATGATAAAAGTTGTTATTGGCGCTTTTGCTTGTTTATTT

SEQ ID NO: 45

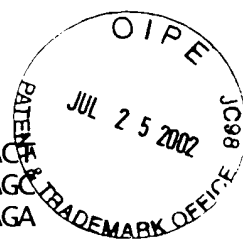
22825 CAATAGTGTGTAACATTAGATGCCATTAGAACCAAAATTGACCATAAGAACCAGAGTTC
AGAAAAATGACTAAGTGTCTTTCATTATGTATTTTCACTCAACATTAGCATTTATGA
AACATTTTGCACATTATCCTGTCCTCACCCTTGCAATGTTACATTTATATAATCTGTGTA
AGTGCTCCACTGCCCCACAGAGTCATAAGTCCCTGGGACTTGGTGATGTGCACAGTGACT
GGCACAGAGGGTGAGCTCTGTCGTGCTTGGGAAGAAAAATGGTCTTCAAATGAATCTTGC
[T,C]

TTGTCTTGAATGTATAAACTGCCTTTTCTAGCAAAAGCATAGACACTCTTCCCTTGGT
GACATGTGCTACGAATTCAGCTGGGTTGAGGATCTGGGCTAAATGAACCAACCTCCCTA
TACATGAAGGATACACAGAGATGGTGACAGAGAGTGGTCACTTCCGTGAGTGGATCTCAA
TCAAGTCTCTGAAGCTAAATTCAATTTTTTTTCTTTACTAAAATGATAAAAGTTGTTAT
TGGCGCTTTTGCTTGTTTATTTTCGTATAACTTAGGGCTCAGATTTTCAATGTGTCAAATG

SEQ ID NO: 46

22967 CCTCACCCTTGCAATGTTACATTTATATAATCTGTGTAAGTGCTCCACTGCCCCACAGAG
TCATAAGTCCCTGGGACTTGGTGATGTGCACAGTGACTGGCACAGAGGGTGAGCTCTGTC

FIGURE 3W



GTGCTTGGGAAGAAAAATGGTCTTCAAATGAATCTTGCCTTGTCTTGAAATGTATAAACT
GCCTTTTCTAGCAAAAGCATAGACACTCTTCCCTTGGTGACATGTGCTACGAATTCAGC
TGGGTTGAGGATCTGGGCTAAATGAACCAAACCTCCCTATACATGAAGGATACACAGAGA
[A,T]

GGTGACAGAGAGTGGTCACTTCCGTGAGTGGATCTCAATCAAGTCCTCTGAAGCTAAATT
CAATTTTTTTCTTTACTAAAATGATAAAAGTTGTTATTGGCGCTTTTGCTTGTTTATTT
CGTATAACTTAGGGCTCAGATTTTCAATGTGTCAAATGCTGACTCACAGCATGGTTCTCC
TGACAGTTTATTTTCAATTAAGGAACTCTTACCAGTAAGTTTATTTACTTGCCTTGATAT
CTCCACACATTAATAATAAACTAACAAAACCTAATCTGAATTAATCTATCAGCTTTA

SEQ ID NO: 47

23248 CATGAAGGATACACAGAGATGGTGACAGAGAGTGGTCACTTCCGTGAGTGGATCTCAATC
AAGTCCTCTGAAGCTAAATTCAATTTTTTTCTTTACTAAAATGATAAAAGTTGTTATTG
GCGCTTTTGCTTGTTTATTTCTGATAACTTAGGGCTCAGATTTTCAATGTGTCAAATGCT
GACTCACAGCATGGTTCTCCTGACAGTTTATTTTCAATTAAGGAACTCTTACCAGTAAGT
TTATTTACTTGCCTTGATATCTCCACACATTAATAATAAACTAACAAAACCTAATCTGA
[A,G]

TTAAAATCTATCAGCTTTAGGCATTATTTTGTGTTCTCCTTCTTTCAACATGGTAACTGG
GCTCTCTTTCTTAGGAGCTTGAGAAGATATGACTGGGGTTTGTCTTCTACTTCATTT
ATTATCTTTCTTTTCCAATCAGTTAGTTTTTCTTTTCTTTAGTAAAAGGTGCATAGTA
ACTGCTTGAGTATTTGTTGAACAAGTGAATAAATGAAATGAATTAAGGTAGTGTCTTCA
CTAGCAGCCCAACATTTCTTTCTCTTAGTAGTGGGTGGGTATCAGTTATGGAATGGC

SEQ ID NO: 48

23764 GAAATGAATTAAGGTAGTGTCTTCACTAGCAGCCCAACATTTCTTCTCTTAGTAGTG
GGTGGGGTATCAGTTATGGAATGGCACCTCCTCCAGAGGACTGATCATGTCAATTTTCAG
CTTATGCTTCCCTTTATGCAGTAAAGTTTCCATATTTCCATAAAGAACAAGAAACCAAAT
AATCCTAATGGATATATAATGAACACACAGATGAAAATTTACCTGCCATGCCTTTGAAA
AAAGATCCCTAGCTACTTGTATTTTCTCTTATAATTAATTAATCAGTCTTTTCACTTATGTT
[G,T]

TCTTCAGATCTCCTGTTTTGAAGTGTATATAGATATCAACATAGAAATGCAGCGTATATT
GCTATCAACTGCAGTGGAGCAGTGATTCTGAGTTTTCCAACATCCTTGCCTTAAGCAAA
CCTGCAAAATCAAAGTGTGAGCTACGTCTAAACAATGGGAGAGGCTTTTTTTTTTTTTTT
AAGAGTTAGAATAAGACTCTCACTTCCTCCTGTGCCTCCACATTTTGACCTTCACATT
GGGCCCCTGCATCAGAATACAGCACCCCTAACAGGCTCCTGTTCAGGACTCTTCTCTG

SEQ ID NO: 49

23765 AAATGAATTAAGGTAGTGTCTTCACTAGCAGCCCAACATTTCTTCTCTTAGTAGTG
GTGGGGTATCAGTTATGGAATGGCACCTCCTCCAGAGGACTGATCATGTCAATTTTCAGC
TTATGCTTCCCTTTATGCAGTAAAGTTTCCATATTTCCATAAAGAACAAGAAACCAAATA
ATCCTAATGGATATATAATGAACACACAGATGAAAATTTACCTGCCATGCCTTTGAAA
AAGATCCCTAGCTACTTGTATTTTCTCTTATAATTAATTAATCAGTCTTTTCACTTATGTT
[C,T]

CTTCAGATCTCCTGTTTTGAAGTGTATATAGATATCAACATAGAAATGCAGCGTATATTG
CTATCAACTGCAGTGGAGCAGTGATTCTGAGTTTTCCAACATCCTTGCCTTAAGCAAAAC
CTGCAAAATCAAAGTGTGAGCTACGTCTAAACAATGGGAGAGGCTTTTTTTTTTTTTTTA
AGAGTTAGAATAAGACTCTCACTTCCTCCTGTGCCTCCACATTTTGACCTTCACATTG
GGCCCCTGCATCAGAATACAGCACCCCTAACAGGCTCCTGTTCAGGACTCTTCTCTG

SEQ ID NO: 50

24432 GGATGGTGCTGGGGACCTCCCTGACCCACAGCATCTGACCCACATTTCCAGGTTCTAGC
GACTTGTGTGAGTAAAGAAAAAGGCACATAGCTAAGTGGAAGAGCAGATGAGGCTTGGTG
GGAATCAGCCAGTGGTCTGCCCTAGCAAAGTAAACAGAAGTCTGTTGGGGCTTTTGGTCC
TAGGCTCACTACTCAGGGAGGCACTTTAACATGGAATGACCAGCAAGTTTCTTCTGAT
CTTTTCCACCACCACCAAGCCTAGTACCTCCCTCCCTCTTTGCTCTGTTGCTCTCTTC
[A,G]

GGAATGCACTGGAACCACCTTCAGTTCTGTTTGAATTTTCTATTCTTATTTCAGAAA
GAGGAAGAAGCTTTTGATTTACTCCAACCGTTCTACCTATTATTCCCATAACTTTCTG

FIGURE 3X



TGATCTCATATCATTAGGCCAAATGTTAATCTTTCTGGGAGCCAGGAGACTGCTTTTCACA
TTCAGAGGCCCTGGACATATAGGACTGCCTCTAACTCACTCTAACTCAGCTTATTGACTT
GAATGCACCTTTTTTAACAAGTGAATAAAAAACAACTGTGACTATTCTCTGAAAATGAGC

SEQ ID NO: 51

24538

GATGAGGCTTGGTGGGAATCAGCCAGTGGTCTGCCCTAGCAAAGGTAAACAGAACTGCTG
GGGGCTTTTGGTCTAGGCTCACTACTCAGGGAGGCACTTTAACATGGAATGACCAGCAA
GTTTCCTTCTGATCTTTTCCACCACCACACAAGCCTAGTACCTCCCTCCCTCTTTGCT
CTGTTGCTCTCTTCGGGAATGCACTGGAAACCACCTTCAGTTCTGTTTGGAAATTTCTTA
TTCCTTATTGAGAAAGAGGAAGAAGCTTTTGCATTTACTCCAACCGTTCTACCTATTATT
[C,G]

CCATAAACTTTCTGTGATCTCATATCATTAGGCCAAATGTTAATCTTTCTGGGAGCCAGG
AGACTGCTTTTACATTGAGAGGCCCTGGACATATAGGACTGCCTCTAACTCACTCTAACT
CAGCTTATTGACTTGAATGCACCTTTTTTAACAAGTGAATAAAAAACAACTGTGACTATT
CTCTGAAAATGAGCCTATATCTCATACTTATTTATTCTGTTTAACTGTGAAAACAAATT
AAGTCTCTGGCACTATGTATATACCATAAAAAGCTTATTTGTAAGCCTACTAATTGGAC

SEQ ID NO: 52

24693

CCTAGTACCTCCCTCCCTCTTTGCTCTGTTGCTCTCTTCGGGAATGCACTGGAAACCACC
TTCAGTTCTGTTTGGAAATTTTCTATTCTTATTGAGAAAGAGGAAGAAGCTTTTGCATT
TACTCCAACCGTTCTACCTATTATTCCCATAACTTTCTGTGATCTCATATCATTAGGCC
AAATGTTAATCTTTCTGGGAGCCAGGAGACTGCTTTACATTGAGAGGCCCTGGACATAT
AGGACTGCCTCTAACTCACTCTAACTCAGCTTATTGACTTGAATGCACCTTTTTTAACAAG
[T,C]

GACTAAAAAACAACTGTGACTATTCTCTGAAAATGAGCCTATATCTCATACTTATTTAT
TCTGTTTAACTGTGAAAACAAATTAAGTCTCTGGCACTATGTATATACCATAAAAAGC
TTATTTGTAAGCCTACTAATTGGACCAGTTTGGACAATATTGAATAAGCACTAATTGCAG
ATCATAATGTAGAATTATAGGCTGCTGAGGAAAACAATATCACACCATTTGCTTTCCTCA
GTTTCCTTTTGAATGAGTTTCATAATGTTCACTAATCCAATTTTTTAAATCCTTTACA

SEQ ID NO: 53

24819

AACCGTTCTACCTATTATTCCCATAACTTTCTGTGATCTCATATCATTAGGCCAAATGT
TAATCTTTCTGGGAGCCAGGAGACTGCTTTACATTGAGAGGCCCTGGACATATAGGACT
GCCTCTAACTCACTCTAACTCAGCTTATTGACTTGAATGCACCTTTTTTAACAAGTGAATA
AAAAACAACTGTGACTATTCTCTGAAAATGAGCCTATATCTCATACTTATTTATTCTGT
TTAACTGTGAAAACAAATTAAGTCTCTGGCACTATGTATATACCATAAAAAGCTTATT
[C,T]

GTAAGCCTACTAATTGGACCAGTTTGGACAATATTGAATAAGCACTAATTGCAGATCATA
ATGTAGAATTATAGGCTGCTGAGGAAAACAATATCACACCATTTGCTTTCCTCAGTTTCC
TTTTCAGAATGAGTTTCATAATGTTCACTAATCCAATTTTTTAAATCCTTTACAAAGTTA
TTCTTAACTATTTCCAGAGACTATCTGTTTGTCTATTCTAGAAATGAAATGCTTTTCA
AGCCTAAACAGATGGCCTTAATTTTTTGGTGGAGTGGTATGAAAGGAATGTCACATGAGAA

SEQ ID NO: 54

25743

TATCCAGTTACAGCAGCGTAACTTGAGCAGCTGCTGCAAACCTGAGGCTCTCTTGACCTT
CGCCTACTTATTTAGCTGCTAAAATAGGGCTGAAATCTGTCAAGGATCCTGAAGGGAAG
GATAAGATTCCTACTATTCAATTTAATTTAAGCTTTTATTGAGTGCCTGCTGTGTGCACA
ACACTAAGCTAGAAAGTCTGAGGAATGTTTAGATTATTAGGTCTGTTCTTGCCTTTCA
TAGATTTACAATCTATTGATAGGGAGAGCTAAAAAGGAGAGAAAGAGGAAGGAGCAAACA
[C,T]

AAAAACGTCAAAATTTTTAAATACCATTTTTAAATTTTTATTTTAAATGTTAAATACCAT
GCAAAATTAAGGAAAACCTAGATTTCATAAAAATTCCTTTTCAATCTTGTGTAAATCAAT
TCAGTGCTTGCCCTTAATGTCTCATCCAGTCTGATGAGACATGTTTTGTGATCAACAAGG
GTTTTACTATGTTTCTAATTATGTGTCTTGCCTGTTATCTCTTTCTGACCGAGATTATT
TTTAAACAATAAATTCTGAAAACCTAAGAAAGTGAAGCATAAAATATTGCTTATATAAATA

SEQ ID NO: 55

26044

AAAAACGTCAAAATTTTTAAATACCATTTTTAAATTTTTATTTTAAATGTTAAATACCAT
GCAAAATTAAGGAAAACCTAGATTTCATAAAAATTCCTTTTCAATCTTGTGTAAATCAAT

FIGURE 3Y



TCAGTGCTTGCCCTTAATGTCTCATCCAGTCTGATGAGACATGTTTTGTGATCAACAAGG
GTTTTACTATGTTTCTTAATTATGTGTCTTGCCTGTTATCTCTTTCTGACCGAGATTATT
TTTAACAATAAATTCTGAAAACCTAAGAAAGTGAAAGCATAAAATATTGTCTTATAAAAATA
[G,C]

GCCAAGGAAAAAATGACACTCCATTTCAAATATCAAAAGTTAGCATCAAGACTGCACAAG
ATGAATGTACAGTCATGTGTTGCTTACAAATGTGGACATATTCTGAGAAATGCATCTTTA
GGCAATTTTGTCAATTGTGCAAAACCCATAGATTGTACTTGCAGCCTAATTGGTGGAGCCT
ACTATACACTAAGGCTATATGGCATAGCCTAGTACTCCTAGGCTACAAACCTGTACAGCA
TGTTACTGTACTGAATAGTGGAGGTACCTGTAAACATAATGGTAAGTATTTGTGTCTCCAA

SEQ ID NO: 56

26555 AGTACTCCTAGGCTACAAACCTGTACAGCATGTTACTGTACTGAATAGTGGAGGTACCTG
TAACATAATGGTAAGTATTTGTGTCTCCAAACGTAGAAAAGCTACTGTAAAAATACAGTA
TTACAACCTTAGGGTATCACTGTCTTATATGTGGTCTGTTGTTGACCGAAATGACTATGC
TTAATACCACTGAAGTGTACACTTAAAAATGGTTAAGATGGTAAATCTATGTTATGTAT
GTTTTATAATAATAAAAAAATTGAAAAAAGCATCAACATCTTTCTGGGAAAAAAGAAAA
[G,A]

GAAAGAAAATGCATTAGAGTGATGAGAATATTTGAAGTAATAGATAAAGTCAAAAAACAA
GAAATGATCTTGCCTTTGAACCTTCTGTTAAGATTCGTACATCAGTGATCACACTGTT
ATTTCCCAAACGACCCTTCAGCTGGATACGACATTTCTGATTGCAGCTGTGCTTATTGC
ACTTAATAATGTTCTGGTCATCCTTGTGCCAACTATAAAATACATCTTCGGATTCATAGG
TGAGTTTCAGAAAGGCTTCAATTTGGTCAACCCAAACTCACGCTCATTAAATGATGGAC

SEQ ID NO: 57

27886 GGTTTATTTAAAGTGTGTGCTGGCATCTCCTTTGCTAGGAACTGCTGGGTAAGACATTGA
CCTTGCCCTGTGTTTGTCTTCTCAGGGGCTTCTTCTGCCACTATGCTGATTTTTATTCTT
CCAGCAGTTTTTTATCTTAACTTGTCAAGAAAGAACTTTTAGGTACCCCCAAAAGGTC
GGGGTAAGTAAACCTTGCAATTTCCCCCATTATTAGTTGTTCTTCAACTACTTAGAATA
AACTAGAAAATACACATAGTTCAGAAAAATGAATCAATGTACAAGAACCAAAAATCAAAA
[A,C]

TGGGCTAGAACTTTCTGGTAGCAGAGAAAGGGGACATATTTCTGAAACTCAAATGATTCT
ACTTCAAATATCAAATATCCTGTGTTGAGTCTGTCATACATGTCAAATAGTAGTAGCCTT
TCCCACAGACACATATGCTTCAGGCAAATAGCAGTGTCCAATACCAAGCTGCTGTTGTGC
TATCCGTGGAAGTATCATGCAAGAAGGAATTAGGCTCCCTAGCGGTGTTATGGAATAATTT
AAATATTTTGGTCATGGTTGTTAGGTTTGCAAAGCCAAAGGAAAGATGTTGCTTTTGTGTT

SEQ ID NO: 58

31884 CTTTTATGGTAGTTTGAAAGAATCCATTGAAGATAGAAAATGAGAGAATAGAAGAAACC
TGAGAATAGTAAAATAAAGAGCAGAGAAAATATGGGGGCAGGGAAAAACATGTGAGTGCTA
AGGATTGATTATGAATGAACGATTAGGGGGATTGATGGATCACAGGGTAAGTATATGCTT
AACTTTATAAGAACTTCCACATAGTTTTCCACAGTGTCTTACCATTTTCATTTCCACC
CGTACTACCTACAACCTTCACTGACTCCACAGCCCTGCCAACATTTGGTGTTGTCTTTTG
[T,C]

ATTTTAGCCTTTCTAGTGGGTCTGAAATGGTAACTCATTGTGATTTTCATTTCTGCTTCT
GTGACAACTAATGTTGAAAACCTTTCAAGTGTTTAAATGGTCACTCATATATCTTCTTTTG
TGAAGTGTGATTCAAATCTTTTGCCATTTTAAAATTTAGGTTATGTGTTTTATTGG
GTATTTGTAGAAGCTCTTAAATATGGATCCATGTCCAGATTGCCAATATATTTCCAG
TCTATGGTATGGTTGCTTATTTTCTAAAGGTGTCTTAATTACATCTTTCTGGGGCCAGG

SEQ ID NO: 59

32229 TTTCAATTTCTGCTTCTGTGACAACTAATGTTGAAAACCTTTCAAGTGTTTAAATGGTCACT
CATATATCTTCTTTTGTGAAGTGTGATTCAAATCTTTTGCCATTTTAAAATTTAGGT
TATGTGTTTTTATTGGGTATTTGTAGAAGCTCTTAAATATGGATCCATGTCCAGATTGC
CAATATATTTTCCAGTCTATGGTATGGTTGCTTATTTTCTAAAGGTGTCTTAATTACA
TCTTTCTGGGGCCAGGTCAACATAGCTCAAAGTTTGCAATTTATGTCTTAATGAGATAA
[T,A]

ATTAATCAGAGTGGTATAGTCAAAATTAATGTTTTGATGTCTGGGCCCATATAGGTAG
GACTGGATCATCTAACCAAGATGCAAAAAAAAAAAAAACAAAAAATAGTACTTG

FIGURE 3Z

Docket No.: CL001010

Serial No.: 09/776,705

Inventor: Karl GUEGLER et al.

Title: ISOLATED HUMAN TRANSPORTER PROTEINS...



GAAAACTTATTTTAAATTAAACA

SEQ ID NO: 60

FIGURE 3AA